STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 115800

TO: Diana Johannsen
Location:
Art Unit: 1634
March 3, 2004

Case Serial Number: 692077

JC10
2C55

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

Sheppard, Paula

From: Johannsen, Diana
Sent: Wednesday, February 25, 2004 11:53 AM
To: Sheppard, Paula
Subject: RE: 09/692,077

Hi Paula:

The search results I received in this case did not include this portion of the search:

nucleotides 880-930 of SEQ ID NO: 1
nucleotides 880-930 of SEQ ID NO: 2

I really need this part of the search since the applicant's polymorphism is located in this region. Could you check to see if this portion of the search was simply not printed or not delivered?

Thanks - I appreciate your help.

Diana

-----Original Message-----
From: Sheppard, Paula
Sent: Tuesday, February 17, 2004 2:18 PM
To: Johannsen, Diana
Subject: RE: 09/692,077

Completed today.

01/06
2/17/04

-----Original Message-----
From: Johannsen, Diana
Sent: Tuesday, February 17, 2004 10:02 AM
To: Sheppard, Paula
Subject: FW: 09/692,077

Hello Paula -

Could you respond to this if possible? Any info would be appreciated (just trying to determine whether I can work on this one this biweek).

Thanks a lot.

-----Original Message-----
From: STIC-Biotech/ChemLib
Sent: Tuesday, February 17, 2004 10:01 AM
To: Johannsen, Diana
Subject: RE: 09/692,077

Check with Paula Sheppard.

-----Original Message-----
From: Johannsen, Diana
Sent: Tuesday, February 17, 2004 9:54 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09/692,077

If possible, could you give me an estimate re: when this search might be complete?

Thank you very much, Diana

-----Original Message-----
From: Johannsen, Diana
Sent: Friday, February 06, 2004 12:04 PM
To: STIC-Biotech/ChemLib
Subject: 09/692,077

Please search the following:

Sheppard
2/3/04

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 04:47:22 ; Search time 864.5 Seconds
(without alignments)
2556.963 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		51	100.0	885	9	HUMA2C2	M38742 Human alpha
2	c	51	100.0	1030	9	HSA325747	AJ325747 Homo sapi
3		51	100.0	1353	6	AX350489	AX350489 Sequence
4		51	100.0	2072	6	AR270618	AR270618 Sequence
5		51	100.0	2072	9	HUMADRA2RA	M34041 Human alpha
6		51	100.0	3274	6	AX548756	AX548756 Sequence
7		51	100.0	9944	9	AF005900	AF005900 Homo sapi
8		43.6	85.5	133405	10	AL662790	AL662790 Mouse DNA
9	c	43.6	85.5	216444	2	AC069060	AC069060 Mus muscu
10		43.4	85.1	1185	10	ASP427259	AJ427259 Anomaluru
11		43.2	84.7	1183	4	OCAAR2B	Y15946 Oryctolagus
12		43.2	84.7	1183	4	OCY16189	Y16189 Oryctolagus
13	c	43.2	84.7	206933	2	AC108794	AC108794 Mus muscu
14		43.2	84.7	215065	2	AC103291	AC103291 Rattus no
15		43.2	84.7	222507	2	AC112440	AC112440 Rattus no
16		43.2	84.7	226214	2	AC126653	AC126653 Rattus no
17		43.2	84.7	287497	2	AC106946	AC106946 Rattus no
18		43.2	84.7	293183	2	AC095903	AC095903 Rattus no
19		43	84.3	1191	10	CCA427260	AJ427260 Castor ca
20	c	42.6	83.5	217323	2	AC115724	AC115724 Mus muscu
21		42.6	83.5	232202	2	AC115740	AC115740 Mus muscu
22	c	42.2	82.7	31533	10	BX465209	BX465209 Mouse DNA
23	c	42.2	82.7	186272	10	AL672046	AL672046 Mouse DNA
24		42.2	82.7	189624	2	AC128836	AC128836 Rattus no
25	c	42.2	82.7	189886	2	AC128202	AC128202 Rattus no
26		42.2	82.7	230127	10	AL691481	AL691481 Mouse DNA
27		42.2	82.7	230227	2	AC112634	AC112634 Rattus no
28		42.2	82.7	230313	2	AC120625	AC120625 Rattus no
29	c	42.2	82.7	268151	2	AC111391	AC111391 Rattus no
30		42	82.4	1198	4	ECAAR2B	Y15945 Equus cabal
31	c	42	82.4	185321	2	AC110324	AC110324 Rattus no
32	c	42	82.4	186607	2	AC140777	AC140777 Mus muscu
33	c	42	82.4	221135	2	AC097027	AC097027 Rattus no
34	c	42	82.4	225928	2	AC128094	AC128094 Rattus no
35		42	82.4	237322	2	AC123153	AC123153 Rattus no
36	c	42	82.4	275192	2	AC119508	AC119508 Rattus no
37		41.6	81.6	309	10	MUSTCE	M17284 Mouse trans
38		41.6	81.6	1197	4	MTE505820	AJ505820 Manis tet
39		41.6	81.6	30837	2	AC126874_4	Continuation (5 of
40	c	41.6	81.6	42003	2	AC145716	AC145716 Homo sapi
41	c	41.6	81.6	42920	2	AC145702	AC145702 Homo sapi
42		41.6	81.6	49999	6	AX015902	AX015902 Sequence
43		41.6	81.6	49999	6	AX015908	AX015908 Sequence
44	c	41.6	81.6	68233	6	AX695956	AX695956 Sequence
45	c	41.6	81.6	78449	2	AC141965	AC141965 Rattus no

ALIGNMENTS

RESULT 1
HUMA2C2
LOCUS HUMA2C2 885 bp DNA linear PRI 06-MAR-1995
DEFINITION Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
ACCESSION M38742
VERSION M38742.1 GI:177867
KEYWORDS alpha-2 adrenergic receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 885)
AUTHORS Chang,A.C., Ho,T.F. and Chang,N.C.
TITLE In vitro amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in

humans
JOURNAL Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
MEDLINE 91054503
PUBMED 2173582
COMMENT Original source text: Human adult neuroblastoma DNA, clone PCRA2.
Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience
155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.

FEATURES Location/Qualifiers
source 1. .885
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="4p16.3-p15"
/clone="PCRA2"
/cell_line="neuroblastoma SK-N-SH"
/cell_type="neuroblastoma"
/tissue_type="neural"
/dev_stage="adult"
gene 1. .885
/gene="ADRA2C"
CDS 1. .885
/gene="ADRA2C"
/codon_start=1
/product="alpha-2-adrenergic receptor"
/protein_id="AAA62823.1"
/db_xref="GI:177868"
/db_xref="GDB:G00-120-540"
/translation="FCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWL
IAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIY
LIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKSTG
EKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEEECEP
QAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFT
FVLAVVIGVFVLCWFPFFF"
ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 885;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 51
Db 598 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 648

RESULT 2
HSA325747/c
LOCUS HSA325747 1030 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, clone NB1-818S.
ACCESSION AJ325747
VERSION AJ325747.1 GI:15870141
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1030)
AUTHORS Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 1030)
AUTHORS Zabarovsky,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

FEATURES Location/Qualifiers
source 1. .1030
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NB1-818S"
ORIGIN

Query Match 100.0%; Score 51; DB 9; Length 1030;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 51
Db 199 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 149

RESULT 3
AX350489
LOCUS AX350489 1353 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liggett,S.B. and Small,K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)

FEATURES Location/Qualifiers
source 1. .1353
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 51
Db 880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 930

RESULT 4
AR270618
LOCUS AR270618 2072 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1181 from patent US 6500938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-DEC-2002;

FEATURES Location/Qualifiers
source 1. .2072
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 2072;

```
  Best Local Similarity   100.0%;  Pred. No. 0.0016;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1342


RESULT 5
HUMADRA2RA
LOCUS       HUMADRA2RA              2072 bp    DNA     linear   PRI 30-OCT-1994
DEFINITION  Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION   M34041
VERSION     M34041.1  GI:178197
KEYWORDS    alpha-2-adrenergic receptor; plasma membrane protein;
            receptor-coupled G protein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2072)
  AUTHORS   Lomasney,J.W., Lorenz,W., Allen,L.F., King,K., Regan,J.W.,
            Yang-Feng,T.L., Caron,M.G. and Lefkowitz,R.J.
  TITLE     Expansion of the alpha 2-adrenergic receptor family: cloning and
            characterization of a human alpha 2-adrenergic receptor subtype,
            the gene for which is located on chromosome 2
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
  MEDLINE   90311349
   PUBMED   2164221
COMMENT     Original source text: Human placenta DNA, clone alpha-2 C2.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by J.W.Lomasney, 03-MAY-1990, for release after publication.
FEATURES             Location/Qualifiers
     source          1. .2072
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="2"
     gene            413. .1765
                     /gene="ADRA2B"
     CDS             413. .1765
                     /gene="ADRA2B"
                     /note="alpha-2-adrenergic receptor (alpha-2 C2)  old gene
                     name 'ADRA2RL1'"
                     /codon_start=1
                     /protein_id="AAA51666.1"
                     /db_xref="GI:178198"
                     /db_xref="GDB:G00-120-539"
                     /translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
                     APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
                     LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRG
                     RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
                     KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
                     LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
                     VLATLRGQVLLGRGVGAIGGQWWRRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSYS
                     LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                     "
ORIGIN      Chromosome 2.

  Query Match             100.0%;  Score 51;  DB 9;  Length 2072;
  Best Local Similarity   100.0%;  Pred. No. 0.0016;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1342


RESULT 6
AX548756
LOCUS       AX548756                3274 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 41 from Patent WO02061087.
ACCESSION   AX548756
VERSION     AX548756.1  GI:25813686
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 41 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .3274
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 3274;
  Best Local Similarity   100.0%;  Pred. No. 0.0016;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930


RESULT 7
AF005900.
LOCUS       AF005900                9944 bp    DNA     linear   PRI 05-AUG-2003
DEFINITION  Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
            complete cds.
ACCESSION   AF005900
VERSION     AF005900.2  GI:33439705
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 9944)
  AUTHORS   Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.,
            Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.
  TITLE     Alpha2C2-adrenergic receptor gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9944)
  AUTHORS   Cayla,C., Schaak,S., Bouloumie,A., Devedjian,J.C. and Paris,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
            CHU Rangueil, Toulouse 31403, France
REFERENCE   3  (bases 1 to 9944)
  AUTHORS   Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.,
            Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-AUG-2003) INSERM Unit 317, Institut Louis Bugnard,
            CHU Rangueil, Toulouse 31403, France
  REMARK    Sequence update by submitter
COMMENT     On Aug 5, 2003 this sequence version replaced gi:2245627.
FEATURES             Location/Qualifiers
     source          1. .9944
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone_lib="brain fetal genomic library"
     gene            5500. .6852
                     /gene="alpha2C2AR"
                     /note="alpha2C2 adrenergic receptor gene"
     CDS             5500. .6852
                     /gene="alpha2C2AR"
                     /note="adrenergic receptor"
                     /codon_start=1
```

```
                     /product="alpha2B-adrenergic receptor"
                     /protein_id="AAB62558.1"
                     /db_xref="GI:2245628"
                     /translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
                     APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
                     LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRG
                     RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
                     KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
                     LPNSGQGQKEGVCGASPEDEAEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
                     VLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
                     LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                     "
     polyA_signal    8751. .8756
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 9944;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6379 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 6429


RESULT 8
AL662790
LOCUS       AL662790               133405 bp    DNA     linear   ROD 26-JUL-2002
DEFINITION  Mouse DNA sequence from clone RP23-53E2 on chromosome 11, complete
            sequence.
ACCESSION   AL662790
VERSION     AL662790.21  GI:22002673
KEYWORDS    HTG.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 133405)
  AUTHORS   Smith,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jul 29, 2002 this sequence version replaced gi:21955513.
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            --------------
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-53E2 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6.
FEATURES             Location/Qualifiers
     source          1. .133405
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="11"
                     /clone="RP23-53E2"
                     /clone_lib="RPCI-23"
ORIGIN

  Query Match             85.5%;  Score 43.6;  DB 10;  Length 133405;
  Best Local Similarity   92.0%;  Pred. No. 0.091;
  Matches   46;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTG 50
              ||||| ||||  ||||||||||||||||||||||||||||||||||| |||
Db       9337 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGTGTG 9386


RESULT 9
AC069060/c
LOCUS       AC069060               216444 bp    DNA     linear   HTG 18-MAR-2003
DEFINITION  Mus musculus chromosome 11 clone RP23-53E2 map 11, WORKING DRAFT
            SEQUENCE, 6 unordered pieces.
ACCESSION   AC069060
VERSION     AC069060.4  GI:29029385
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 216444)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus chromosome 11, clone RP23-53E2
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 216444)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
            Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
            Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
            Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
            Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
            McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
            Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
            Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
            Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
            Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 216444)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
            Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
            Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
            Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
            Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
            Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
            Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
            Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
            Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
            Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
            Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
```

```
            Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
            Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
            Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
            Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
            Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-MAR-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 18, 2003 this sequence version replaced gi:15291107.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L9470
                Center clone name: 53_E_2
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 25% of reads
                Sequencing vector: Plasmid; n/a; 75% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 215352 bases at least Q40
                Consensus quality: 215747 bases at least Q30
                Consensus quality: 215851 bases at least Q20
                Insert size: 215944; sum-of-contigs
                Quality coverage: 12.0 in Q20 bases; sum-of-contigs
            --------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 6 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    12827: contig of 12827 bp in length
            *    12828    12927: gap of 100 bp
            *    12928    16683: contig of 3756 bp in length
            *    16684    16783: gap of 100 bp
            *    16784    25277: contig of 8494 bp in length
            *    25278    25377: gap of 100 bp
            *    25378    40696: contig of 15319 bp in length
            *    40697    40796: gap of 100 bp
            *    40797   138890: contig of 98094 bp in length
            *   138891   138990: gap of 100 bp
            *   138991   216444: contig of 77454 bp in length.
FEATURES             Location/Qualifiers
     source          1. .216444
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /chromosome="11"
                     /map="11"
                     /clone="RP23-53E2"
                     /clone_lib="RPCI-23 Female Mouse BAC"
     misc_feature    1. .12827
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    12928. .16683
                     /note="assembly_fragment"
     misc_feature    16784. .25277
                     /note="assembly_fragment"
     misc_feature    25378. .40696
                     /note="assembly_fragment"
     misc_feature    40797. .138890
                     /note="assembly_fragment"
     misc_feature    138991. .216444
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             85.5%;  Score 43.6;  DB 2;  Length 216444;
  Best Local Similarity   92.0%;  Pred. No. 0.088;
  Matches   46;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTG 50
              ||||| |||| ||||||||||||||||||||||||||||||||||| |||
Db     207108 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGTGTG 207059


RESULT 10
ASP427259
LOCUS       ASP427259               1185 bp    DNA     linear   ROD 06-AUG-2003
DEFINITION  Anomalurus sp. partial A2AB gene for alpha 2B adrenergic receptor,
            exon 1.
ACCESSION   AJ427259
VERSION     AJ427259.1  GI:21655549
KEYWORDS    A2AB gene; alpha 2B adrenergic receptor.
SOURCE      Anomalurus sp.
  ORGANISM  Anomalurus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Anomaluridae;
            Anomalurus.
REFERENCE   1
  AUTHORS   Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J.,
            Catzeflis,F., de Jong,W.W. and Douzery,E.J.
  TITLE     Rodent phylogeny and a timescale for the evolution of Glires:
            evidence from an extensive taxon sampling using three nuclear genes
  JOURNAL   Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
  MEDLINE   22077630
   PUBMED   12082125
REFERENCE   2
  AUTHORS   Douzery,E.J.P., Delsuc,F., Stanhope,M.J. and Huchon,D.
  TITLE     Local molecular clocks in three nuclear genes: divergence times for
            rodents and other mammals, and incompatibility among fossil
            calibrations
  JOURNAL   J. Mol. Evol. (2003) In press
REFERENCE   3  (bases 1 to 1185)
  AUTHORS   Douzery,E.J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences de
            l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite
            Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
            FRANCE
FEATURES             Location/Qualifiers
     source          1. .1185
                     /organism="Anomalurus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:101665"
     gene            1. .1185
                     /gene="A2AB"
     CDS             <1. .>1185
                     /gene="A2AB"
                     /codon_start=1
                     /product="alpha 2B adrenergic receptor"
                     /protein_id="CAD20297.1"
                     /db_xref="GI:21655550"
                     /db_xref="GOA:Q8K3R6"
                     /db_xref="SPTREMBL:Q8K3R6"
                     /translation="AIAAVTTFLILFTIFGNALVILAVLTSHSLRAPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFWSTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
                     RALEYNSKRTPRRIKRIILIVWLIAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYI
                     LASSIGSFFAPCLIMILVYLRIYVIAKRSNRRGPRTNGRPGQGESKQFPPVPGGAPAS
                     AKVPTLSSPLSSAGEANGHPKPPGEKEDGETPEDPGARALPSSWAALPNSGQGQKKGA
                     CGASAEEEAEEEEEEEEEECEPQAVPVSPASVCSQPLQQPQGSRVLATLRGQVLLGR
                     HVGTAGGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPH
                     GLF"
     exon            <1. .>1185
                     /gene="A2AB"
```

```
ORIGIN              /number=1

  Query Match              85.1%;  Score 43.4;  DB 10;  Length 1185;
  Best Local Similarity    97.8%;  Pred. No. 0.14;
  Matches   44;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAA 45
              ||||| ||||||||||||||||||||||||||||||||||||||||
Db        844 GAGGAGGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAA 888


RESULT 11
OCAAR2B
LOCUS       OCAAR2B                1183 bp    DNA     linear   MAM 15-NOV-1999
DEFINITION  Oryctolagus cuniculus gene encoding alpha adrenergic receptor
            subtype 2B, partial.
ACCESSION   Y15946
VERSION     Y15946.2  GI:6448590
KEYWORDS    alpha adrenergic receptor; subtype 2B.
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Stanhope,M.J., Madsen,O., Waddell,V.G., Cleven,G.C., de Jong,W.W.
            and Springer,M.S.
  TITLE     Highly congruent molecular support for a diverse superordinal clade
            of edemic African mammals
  JOURNAL   Unpublished
REFERENCE   2
  AUTHORS   Madsen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-DEC-1997) O. Madsen, University of Nijmegen,
            Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
            NETHERLANDS
  REMARK    Revised by [3]
REFERENCE   3  (bases 1 to 1183)
  AUTHORS   Madsen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
            Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
            NETHERLANDS
COMMENT     On Nov 17, 1999 this sequence version replaced gi:3288559.
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="Oryctolagus cuniculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9986"
     CDS             <1. .>1183
                     /codon_start=2
                     /product="alpha adrenergic receptor subtype 2B"
                     /protein_id="CAA75899.2"
                     /db_xref="GI:6448591"
                     /db_xref="GOA:O77830"
                     /db_xref="SWISS-PROT:O77830"
                     /translation="AIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
                     RALEYNCKRTPRRIKCIILTVWLIAAAISLPPLIYKGDQGPQPHGAPQCKLNQEAWYI
                     LSSSLGSFFVPCLIMILVYLRIYLIAKRSHRRGPRAKGGPGEGESRQACPVPGGPSAS
                     AKLPTLATPVASASEANGPSKPAGEKEEGETPEDPGTQALPPGWATLPNSGQGQKEGV
                     SGASLEEEAEEEEEEEEEEDEPQAVPVSPASVGSPPLQQPQGSRVLATLRGQVLVGRG
                     VGAMSGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
                     LF"
ORIGIN

  Query Match              84.7%;  Score 43.2;  DB 4;  Length 1183;
  Best Local Similarity    93.8%;  Pred. No. 0.15;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||||||||||||||| |||||||||||||||||||||| |||
Db        845 GAGGAAGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGAG 892


RESULT 12
OCY16189
LOCUS       OCY16189               1183 bp    DNA     linear   MAM 02-JUL-1998
DEFINITION  Oryctolagus cuniculus gene encoding alpha adrenergic receptor
            subtype 2B, partial.
ACCESSION   Y16189
VERSION     Y16189.1  GI:3288561
KEYWORDS    alpha adrenergic receptor.
SOURCE      Oryctolagus cuniculus (rabbit)
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Stanhope,M.J., Madsen,O.J., Waddell,V.G., Cleven,G.C., de Jong,W.W.
            and Springer,M.S.
  TITLE     Highly congruent molecular support for a diverse superordinal clade
            of edemic African mammals
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1183)
  AUTHORS   Madsen,O.O.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JAN-1998) O.O.M. Madsen, University of Nijmegen,
            Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
            NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1183
                     /organism="Oryctolagus cuniculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9986"
     CDS             <1. .>1183
                     /codon_start=2
                     /product="alpha adrenergic receptor subtype 2B"
                     /protein_id="CAA76115.1"
                     /db_xref="GI:3288562"
                     /db_xref="GOA:O77830"
                     /db_xref="SWISS-PROT:O77830"
                     /translation="AIAAVITFLILFTIFGNALVILAVLTSRSLRXPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFRRTWXXVYLALDVLFCTSSIVHLCAISLDRYXAVS
                     RALEYNXKRTPRRIKCIILTVWLIAAAISLPPLIYKGDQGPQPHGAPQCKLNQEAWYI
                     LSSSLGSFFVPCLIMILVYLRIYLIAKRSHRRGPRAKGGPGEGESRQACPVPGGPSAS
                     AKLPTLATPVASASEANGPSKPAGEKEEGETPEDPGTQALPPGWATLPNSGQGQKEGV
                     SGASLEEEAEEEEEEEEEEDEPQAVPVSPASVGSPPLQQPQGSRVLATLRGQVLVGRG
                     VGAMSGXWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLSAICPQQCRVPHG
                     LF"
ORIGIN

  Query Match              84.7%;  Score 43.2;  DB 4;  Length 1183;
  Best Local Similarity    93.8%;  Pred. No. 0.15;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||||||||||||||| |||||||||||||||||||||| |||
Db        845 GAGGAAGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGACGAG 892


RESULT 13
AC108794/c
LOCUS       AC108794               206933 bp    DNA     linear   HTG 22-OCT-2002
DEFINITION  Mus musculus clone RP23-59D8, WORKING DRAFT SEQUENCE, 10 ordered
            pieces.
ACCESSION   AC108794
VERSION     AC108794.4  GI:24211386
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 206933)
  AUTHORS   Birren,B., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP23-59D8
  JOURNAL   Unpublished
```

```
REFERENCE   2  (bases 1 to 206933)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
            Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C.,
            Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
            McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
            Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
            Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
            Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE   3  (bases 1 to 206933)
  AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,
            Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
            Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
            Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
            Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
            Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
            Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Oct 22, 2002 this sequence version replaced gi:20336084.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L20652
                Center clone name: 59_D_8
            -------------- Summary Statistics
                Sequencing vector: Plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 204584 bases at least Q40
                Consensus quality: 205483 bases at least Q30
                Consensus quality: 205753 bases at least Q20
                Insert size: 205000; agarose-fp
                Insert size: 206033; sum-of-contigs
                Quality coverage: 10.1 in Q20 bases; agarose-fp
                Quality coverage: 10.1 in Q20 bases; sum-of-contigs
            --------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 10 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    30760: contig of 30760 bp in length
            *    30761    30860: gap of 100 bp
            *    30861    31511: contig of 651 bp in length
            *    31512    31611: gap of 100 bp
            *    31612    36489: contig of 4878 bp in length
            *    36490    36589: gap of 100 bp
            *    36590    77765: contig of 41176 bp in length
            *    77766    77865: gap of 100 bp
            *    77866    91260: contig of 13395 bp in length
            *    91261    91360: gap of 100 bp
            *    91361   111714: contig of 20354 bp in length
            *   111715   111814: gap of 100 bp
            *   111815   134504: contig of 22690 bp in length
            *   134505   134604: gap of 100 bp
            *   134605   165128: contig of 30524 bp in length
            *   165129   165228: gap of 100 bp
            *   165229   197581: contig of 32353 bp in length
            *   197582   197681: gap of 100 bp
            *   197682   206933: contig of 9252 bp in length.
FEATURES             Location/Qualifiers
     source          1. .206933
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="RP23-59D8"
                     /clone_lib="RPCI-23 Female Mouse BAC"
     misc_feature    1. .30760
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
     misc_feature    30861. .31511
                     /note="assembly_fragment"
     misc_feature    31612. .36489
                     /note="assembly_fragment"
     misc_feature    36590. .77765
                     /note="assembly_fragment"
     misc_feature    77866. .91260
                     /note="assembly_fragment"
     misc_feature    91361. .111714
                     /note="assembly_fragment"
     misc_feature    111815. .134504
                     /note="assembly_fragment"
     misc_feature    134605. .165128
                     /note="assembly_fragment"
     misc_feature    165229. .197581
                     /note="assembly_fragment"
     misc_feature    197682. .206933
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
ORIGIN

  Query Match             84.7%;  Score 43.2;  DB 2;  Length 206933;
  Best Local Similarity   93.8%;  Pred. No. 0.11;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              |||||||||| |||||||||||||||||||||||||||||||| |||
Db     174928 GAGGATGAAGAAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGAG 174881


RESULT 14
AC103291
LOCUS       AC103291              215065 bp    DNA     linear   HTG 09-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-131O4, WORKING DRAFT SEQUENCE, 2
```

unordered pieces.
ACCESSION AC103291
VERSION AC103291.5 GI:24819202
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 215065)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215065)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 215065)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 9, 2002 this sequence version replaced gi:23268227.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
---------- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
---------- Project Information
Center project name: GJSU
Center clone name: CH230-131O4
---------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 200859 bases at least Q40
Consensus quality: 202934 bases at least Q30
Consensus quality: 204251 bases at least Q20
Estimated insert size: 207073; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 211244: contig of 211244 bp in length
* 211245 211344: gap of unknown length
* 211345 215065: contig of 3721 bp in length.

FEATURES Location/Qualifiers
source 1. .215065
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-131O4"
misc_feature 1. .1132
/note="wgs_end_extension
clone_end:T7"
misc_feature 2440. .3271
/note="clone_boundary
clone_end:T7
site:EcoRI
end_sequence:BH316900"
misc_feature 202478. .203219
/note="clone_boundary
clone_end:Sp6
site:EcoRI
end_sequence:BH316902"
misc_feature 203592. .205041
/note="wgs_end_extension
clone_end:Sp6"
misc_feature 209692. .211244
/note="wgs_end_extension
clone_end:Sp6"
misc_feature 211345. .212647
/note="wgs_end_extension
clone_end:Sp6"
misc_feature 213358. .215065
/note="wgs_end_extension
clone_end:Sp6"

```
ORIGIN

  Query Match             84.7%;  Score 43.2;  DB 2;  Length 215065;
  Best Local Similarity   93.8%;  Pred. No. 0.11;
  Matches   45;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  ||||||||||||||||||||||||||||||||||||
Db     186041 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 186088


RESULT 15
AC112440
LOCUS       AC112440               222507 bp    DNA     linear   HTG 15-NOV-2002
DEFINITION  Rattus norvegicus clone CH230-144K15, WORKING DRAFT SEQUENCE, 4
            unordered pieces.
ACCESSION   AC112440
VERSION     AC112440.5  GI:25006757
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 222507)
  AUTHORS   Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
            Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
            Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
            Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
            Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
            Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
            Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
            Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
            Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
            Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
            Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
            Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
            Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
            Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
            Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
            Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
            Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
            Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
            Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
            Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
            Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
            Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
            Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
            Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
            Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
            Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
            Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
            Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
            Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
            Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
            Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
            Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
            Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
            Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
            Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
            Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
            Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
            Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
            Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
            Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
            Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
            Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
            Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
            Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
            Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
            Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
            Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
            Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
            Weinstock,G. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 222507)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 222507)
  AUTHORS   Rat Genome Sequencing Consortium.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Nov 15, 2002 this sequence version replaced gi:22856702.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GRYP
                Center clone name: CH230-144K15
            -------------- Summary Statistics
                Assembly program: Phrap; version 0.990329
                Consensus quality: 206932 bases at least Q40
                Consensus quality: 208648 bases at least Q30
                Consensus quality: 209801 bases at least Q20
                Estimated insert size: 210499; sum-of-contigs estimation
                Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    53077: contig of 53077 bp in length
            *    53078    53177: gap of unknown length
            *    53178    57398: contig of 4221 bp in length
            *    57399    57498: gap of unknown length
            *    57499   164797: contig of 107299 bp in length
            *   164798   164897: gap of unknown length
            *   164898   222507: contig of 57610 bp in length.
FEATURES             Location/Qualifiers
     source          1. .222507
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10116"
                     /clone="CH230-144K15"
     misc_feature    1. .1032
                     /note="wgs_contig"
     misc_feature    57499. .58533
                     /note="wgs_contig"
     misc_feature    62821. .64890
                     /note="wgs_contig"
```

misc_feature 109071. .110316
/note="wgs_contig"
ORIGIN

Query Match 84.7%; Score 43.2; DB 2; Length 222507;
Best Local Similarity 93.8%; Pred. No. 0.11;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  ||||||||||||||||||||||||||||||||||||
Db     153574 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 153621
```

Search completed: March 2, 2004, 06:08:05
Job time : 866.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 04:46:17 ; Search time 267.5 Seconds
(without alignments)
809.937 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
	1	51	100.0	1353	4	AAI99905	Aai99905 Human alp
	2	51	100.0	1353	5	AAD04762	Aad04762 Human alp
	3	51	100.0	1353	6	AAD44389	Aad44389 Human alp
	4	51	100.0	2064	2	AAQ14151	Aaq14151 Human alp
	5	51	100.0	2064	2	AAT59499	Aat59499 Human alp
	6	51	100.0	2072	7	ACA56583	Aca56583 Human sig
	7	51	100.0	3274	7	ABZ42624	Abz42624 Human alp
	8	41.6	81.6	291	5	AAS68926	Aas68926 DNA encod
	9	41.6	81.6	49999	2	AAZ23896	Aaz23896 Murine LO
	10	41.6	81.6	49999	2	AAZ23891	Aaz23891 Murine LO
c	11	41.6	81.6	68230	8	ADA66349	Ada66349 Mouse Ppp
c	12	41.6	81.6	68233	8	ADA03065	Ada03065 Mouse Ppp
c	13	41.6	81.6	68233	9	ADB72803	Adb72803 Mouse Ppp
c	14	41.6	81.6	215980	6	AAL38337	Aal38337 Complemen
c	15	40.6	79.6	1721	6	ABQ76418	Abq76418 S. cerevi
	16	40.6	79.6	2663	7	AAD55832	Aad55832 Human nuc
	17	40.2	78.8	1344	5	AAD04761	Aad04761 Human alp
	18	40.2	78.8	1344	6	AAD44388	Aad44388 Human alp
	19	40	78.4	223	7	ABX90802	Abx90802 Murine ge
	20	40	78.4	224	5	AAS75432	Aas75432 DNA encod
c	21	40	78.4	234	6	ABQ98152	Abq98152 Mouse ES
	22	40	78.4	330	7	ABX90780	Abx90780 Murine ge
	23	40	78.4	1173	7	ACD13226	Acd13226 cDNA enco
	24	40	78.4	1178	7	ACD13227	Acd13227 cDNA enco
	25	40	78.4	1956	3	AAC38547	Aac38547 Arabidops
	26	40	78.4	2367	7	ABT20256	Abt20256 Aspergill
	27	40	78.4	2367	7	ABT20854	Abt20854 Aspergill
	28	40	78.4	2663	6	ABK65237	Abk65237 Arabidops
	29	40	78.4	2663	8	ACD98382	Acd98382 A. thalia
	30	40	78.4	2663	9	ADD30227	Add30227 Plant yie
	31	40	78.4	2663	9	ADE37126	Ade37126 Plant yie
	32	40	78.4	4238	7	ABT17846	Abt17846 Aspergill
	33	40	78.4	4367	7	ABT19660	Abt19660 Aspergill
	34	40	78.4	5888	2	AAZ24013	Aaz24013 Human GDN
c	35	39.8	78.0	2013	4	AAK52886	Aak52886 Human pol
c	36	39.8	78.0	2205	4	AAK51902	Aak51902 Human pol
c	37	39	76.5	417	5	AAS92073	Aas92073 DNA encod
	38	39	76.5	417	5	AAS75433	Aas75433 DNA encod
	39	39	76.5	423	4	AAI20873	Aai20873 Probe #10
	40	39	76.5	423	4	ABA65943	Aba65943 Human foe
	41	39	76.5	423	4	AAI46111	Aai46111 Probe #14
	42	39	76.5	423	4	ABA48060	Aba48060 Human bre
	43	39	76.5	423	4	ABA33035	Aba33035 Probe #11
	44	39	76.5	423	4	AAK40093	Aak40093 Human bon
	45	39	76.5	423	4	AAK14364	Aak14364 Human bra

ALIGNMENTS

RESULT 1
AAI99905
ID AAI99905 standard; DNA; 1353 BP.
XX
AC AAI99905;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR;
KW GenBank Accession AF009500; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1353
FT /*tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence includes a 9 nucleotide polymorphic site
FT at nucleotides 901-909 absent in the alpha-2BAR variant
FT (AAI99906)"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US012575.
XX
PR 17-APR-2000; 2000US-00551744.
PR 10-AUG-2000; 2000US-00636259.
PR 19-OCT-2000; 2000US-00692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52117.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a

PT disease associated with the corresponding receptor comprises detecting a
PT polymorphic site.
XX
PS Claim 4; Page 144; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a)
CC obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic
CC site comprising nucleotide positions 901-909 of (I), a site comprising
CC cytosine or guanine at position 753 of (IIV) or a site comprising (A)
CC (ggggcggggccg) or (B) (ggggcggctgag) at positions 961-972 of (III). The
CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
CC gene and further used to determine whether an individual is at increased
CC risk of developing a disease associated with alpha2B, alpha2A or alpha2,
CC comprising detecting a polymorphic site which correlate to disease
CC selected from cardiovascular disease, central nervous system disease and
CC combinations of these. In addition, the technique may be used to predict
CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
CC epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
CC prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and
CC combinations of these) by detecting the polymorphic site and correlating
CC the site to a predetermined response (where the response is correlated to
CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
CC phosphate levels). The present sequence is that of the third
CC intracellular loop of the human alpha-2BAR (GenBank Accession AF009500),
CC the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-
CC 909, absent in the alpha-2BAR variant (AAI99906)
XX
SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 4; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930

RESULT 2
AAD04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heat disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1353
FT /*tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT protein"
XX
PN WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI000913.
XX
PR 22-OCT-1999; 99US-00422985.
XX
PA (JUVA-) JUVANTIA PHARMA LTD OY.
XX
PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssoenen K;
PI Salonen R, Kauhanen J, Valkonen V;
XX
DR WPI; 2001-300318/31.
DR P-PSDB; AAE00990.
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular loop
PT of the polypeptide, for treating vascular contraction of coronary
PT arteries.
XX
PS Disclosure; Page 27-29; 37pp; English.
XX
CC The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311), located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-
CC adrenoceptor is useful for treating a mammal suffering from vascular
CC contraction of coronary arteries and a disease involving vascular
CC contraction of coronary arteries which is clinically expressed as
CC coronary heat disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 5; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930

RESULT 3
AAD44389
ID AAD44389 standard; DNA; 1353 BP.
XX
AC AAD44389;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human alpha-2B-adrenoceptor gene.
XX
KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1353
FT /*tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"
XX
PN WO200266617-A1.
XX
PD 29-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-FI000113.
XX
PR 20-FEB-2001; 2001FI-00000323.
XX
PA (JURI-) JURILAB LTD OY.
XX
PI Salonen J;
XX

```
DR   WPI; 2002-667063/71.
DR   P-PSDB; AAE26634.
XX
PT   Detecting a risk of hypertension and targeting treatment in a subject by
PT   determining the pattern of alleles encoding a variant alpha-2-
PT   adrenoceptor.
XX
PS   Disclosure; Page 27-29; 35pp; English.
XX
CC   The invention relates to a method for detecting a risk of hypertension by
CC   determining the pattern of alleles encoding a variant alpha-2B-
CC   adrenoceptor (AR) protein. The methods and compositions of the invention
CC   are useful for detecting risks and targeting treatment for hypertension.
CC   The kit is also useful for selecting for clinical drug trials testing the
CC   antihypertensive effect of compounds. The present sequence is human alpha
CC   -2B-adrenoceptor gene
XX
SQ   Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 6;  Length 1353;
  Best Local Similarity   100.0%;  Pred. No. 0.00055;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930


RESULT 4
AAQ14151
ID   AAQ14151 standard; DNA; 2064 BP.
XX
AC   AAQ14151;
XX
DT   06-JAN-1992  (first entry)
XX
DE   Human alpha 2 beta adrenergic receptor gene.
XX
KW   Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             288. .1752
FT                   /*tag=  a
XX
PN   US5053337-A.
XX
PD   01-OCT-1991.
XX
PF   30-OCT-1989;   89US-00428856.
XX
PR   30-OCT-1989;   89US-00428856.
XX
PA   (NEUR-) NEUROGENETIC CORP.
XX
PI   Weinshank RL,  Hartig PR;
XX
DR   WPI; 1991-310087/42.
DR   P-PSDB; AAR14149.
XX
PT   Isolated DNA encoding human adrenergic receptor - for detecting nucleic
PT   acids encoding alpha, 2-beta adrenergic receptor, for screening drugs.
XX
PS   Claim 1; Fig 2; 15pp; English.
XX
CC   Clone NGC-alpha2beta was isolated from a human spleen genomic library by
CC   screening with a fragment of the human 5-HT1A receptor gene. The gene can
CC   be used to express recombinant receptor protein which can be used to
CC   produce antibodies for inhibition of receptor function
XX
SQ   Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 2;  Length 2064;
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1328


RESULT 5
AAT59499
ID   AAT59499 standard; DNA; 2064 BP.
XX
AC   AAT59499;
XX
DT   25-MAR-2003  (revised)
DT   06-MAY-1997  (first entry)
XX
DE   Human alpha-2b adrenergic receptor genomic DNA clone.
XX
KW   Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine;
KW   signal transduction; neurotransmitter; ligand; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             288. .1751
FT                   /*tag=  a
XX
PN   US5595880-A.
XX
PD   21-JAN-1997.
XX
PF   22-OCT-1992;   92US-00965040.
XX
PR   30-OCT-1989;   89US-00428856.
PR   30-MAY-1991;   91US-00707604.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Hartig PR,  Weinshank RL;
XX
DR   WPI; 1997-107576/10.
DR   P-PSDB; AAW11804.
XX
PT   Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
PT   expressing recombinant receptor.
XX
PS   Disclosure; Fig 2A-E; 16pp; English.
XX
CC   A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic
CC   receptor (AAW11804), a member of the rhodopsin-like signal transducer
CC   family. It was isolated from a human spleen genomic library in the lambda
CC   vector Charon 28 by screening with a 1.6 kb fragment of the human 5-
CC   hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA
CC   encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors
CC   have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial,
CC   yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-
CC   2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in
CC   novel methods to identify drugs which specifically interact with, and
CC   bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 2;  Length 2064;
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1328
```

RESULT 6
ACA56583
ID ACA56583 standard; cDNA; 2072 BP.
XX
AC ACA56583;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1181; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 7; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1292 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1342

RESULT 7
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP.
XX
AC ABZ42624;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR P-PSDB; ABP81780.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 7; Length 3274;

```
  Best Local Similarity   100.0%;  Pred. No. 0.00056;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930


RESULT 8
AAS68926
ID   AAS68926 standard; cDNA; 291 BP.
XX
AC   AAS68926;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #4730.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US008631.
XX
PR   31-MAR-2000; 2000US-00540217.
PR   23-AUG-2000; 2000US-00649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG04739.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity.
XX
PS   Claim 1; SEQ ID NO 4730; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC   sequences. (I) is useful as hybridisation probes, polymerase chain
CC   reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC   and in recombinant production of (II). The polynucleotides are also used
CC   in diagnostics as expressed sequence tags for identifying expressed
CC   genes. (I) is useful in gene therapy techniques to restore normal
CC   activity of (II) or to treat disease states involving (II). (II) is
CC   useful for generating antibodies against it, detecting or quantitating a
CC   polypeptide in tissue, as molecular weight markers and as a food
CC   supplement. (II) and its binding partners are useful in medical imaging
CC   of sites expressing (II). (I) and (II) are useful for treating disorders
CC   involving aberrant protein expression or biological activity. The
CC   polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC   coding sequences of the invention. Note: The sequence data for this
CC   patent did not appear in the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 291 BP; 129 A; 22 C; 112 G; 28 T; 0 U; 0 Other;

  Query Match           81.6%;  Score 41.6;  DB 5;  Length 291;
  Best Local Similarity   91.7%;  Pred. No. 0.11;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  ||||||||||||||||||| ||||||||||||||||
Db         79 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAAGAGGAGGAGGAAGAG 126


RESULT 9
AAZ23896
ID   AAZ23896 standard; DNA; 49999 BP.
XX
AC   AAZ23896;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Murine LOBO homologue genomic DNA fragment 2.
XX
KW   LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW   diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW   spondyloepiphysal dysplasia; achondroplasia; murine; ds.
XX
OS   Mus musculus.
XX
PN   WO9950284-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-EP002055.
XX
PR   27-MAR-1998;   98DE-01013799.
XX
PA   (ROSE/) ROSENTHAL A.
XX
PI   Rosenthal A,  Rump A,  Hess J,  Aigner T,  Wirth T;
XX
DR   WPI; 1999-601320/51.
XX
PT   Nucleic acids encoding proteins which influence bone development, useful
PT   for treating and studying bone disorders.
XX
PS   Example 3; Page 161-189; 391pp; German.
XX
CC   This invention describes novel nucleic acids (I; designated LOBO (long
CC   bones)) encoding proteins influencing bone development in mammals. The
CC   proteins of the invention reduce and/or inactivate bone extension (i.e.
CC   development), with exception of the skull and have osteopathic activity.
CC   The nucleic acid molecules, proteins and antibodies can be used in
CC   diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
CC   and nucleic acid molecules, etc. are useful for production of transgenic
CC   animals, especially a transgenic mouse for the study of diseases
CC   associated with bone development, e.g. spondyloepiphysal dysplasia and
CC   achondroplasia. This sequence encodes the murine LOBO protein described
CC   in the method of the invention
XX
SQ   Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 U; 0 Other;

  Query Match           81.6%;  Score 41.6;  DB 2;  Length 49999;
  Best Local Similarity   91.7%;  Pred. No. 0.12;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  ||||||||||||||||||| ||||||||||||||||
Db      12384 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAAGAGGAGGAGGAAGAG 12431


RESULT 10
AAZ23891
ID   AAZ23891 standard; DNA; 49999 BP.
XX
AC   AAZ23891;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Murine LOBO genomic DNA fragment 1.
```

XX
KW LOBO; long bones; bone development; bone extension; skull; osteopathic;
KW diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
KW spondyloepiphysal dysplasia; achondroplasia; murine; ds.
XX
OS Mus musculus.
XX
PN WO9950284-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-EP002055.
XX
PR 27-MAR-1998; 98DE-01013799.
XX
PA (ROSE/) ROSENTHAL A.
XX
PI Rosenthal A, Rump A, Hess J, Aigner T, Wirth T;
XX
DR WPI; 1999-601320/51.
XX
PT Nucleic acids encoding proteins which influence bone development, useful
PT for treating and studying bone disorders.
XX
PS Example 3; Page 69-97; 391pp; German.
XX
CC This invention describes novel nucleic acids (I; designated LOBO (long
CC bones)) encoding proteins influencing bone development in mammals. The
CC proteins of the invention reduce and/or inactivate bone extension (i.e.
CC development), with exception of the skull and have osteopathic activity.
CC The nucleic acid molecules, proteins and antibodies can be used in
CC diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
CC and nucleic acid molecules, etc. are useful for production of transgenic
CC animals, especially a transgenic mouse for the study of diseases
CC associated with bone development, e.g. spondyloepiphysal dysplasia and
CC achondroplasia. This sequence encodes the murine LOBO protein described
CC in the method of the invention
XX
SQ Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 2; Length 49999;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
||||| |||| |||||||||||||||||||| ||||||||||||||||
Db 10399 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAGGAAGAGGAGGAGGAAGAG 10446

RESULT 11
ADA66349/c
ID ADA66349 standard; DNA; 68230 BP.
XX
AC ADA66349;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse Ppp3cc gene genomic DNA sequence.
XX
KW carcinoma-associated gene; CA gene; Rorc gene; mCG15938 gene; BAT1 gene;
KW Iqgap1 gene; IQGAP1 gene; Zpf29 gene; hCG27579 gene; Kcnj9 gene;
KW KCNJ9 gene; Ppp3cc gene; PPP3CC gene; mCG9110 gene; hCG27579 gene;
KW cancer cell; lymphatic cell; breast cell; prostate cell; epithelial cell;
KW carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer;
KW vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer;
KW prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Ppp3cc.
XX
OS Mus sp.
XX
PN WO2003053224-A2.
XX
PD 03-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041776.
XX
PR 20-DEC-2001; 2001US-00034650.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
DR WPI; 2003-569168/53.
XX
PT Novel recombinant carcinoma-associated nucleic acid, useful for
PT evaluating the effect of a candidate carcinoma drug, and for diagnosing
PT carcinoma.
XX
PS Claim 1; Page 110-120; 229pp; English.
XX
CC This invention relates to a novel recombinant carcinoma-associated (CA)
CC nucleic acid comprising a fully defined genomic, mRNA or coding sequences
CC of mouse Rorc gene or human RORC gene, mouse mCG15938 or human gene BAT1,
CC mouse Iqgap1 gene or human IQGAP1 gene, mouse Zpf29 gene or human
CC hCG27579 gene, mouse Kcnj9 gene or human KCNJ9 gene, mouse Ppp3cc gene or
CC human PPP3CC gene, mouse mCG9110 gene or human hCG27579 gene, as given in
CC the specification. CA genes are genes which are preferably expressed in
CC cancer cells, preferably lymphatic, breast, prostate or epithelial cells.
CC A compound which modifies the expression of the CA genes or bind to
CC carcinoma-associated proteins (CAP) may have cytostatic activity and the
CC sequences of the invention may enable the use of gene therapy or a
CC development of an anticancer vaccine. Therefore the invention may be
CC useful for diagnosis and treatment of carcinomas, especially lymphoma
CC carcinoma, breast cancer and prostate cancer. The CA genes may also be
CC useful as DNA vaccines and for generating animal models of carcinomas.
CC The present sequence is that of the mouse Ppp3cc gene genomic DNA
CC sequence of the invention.
XX
SQ Sequence 68230 BP; 18765 A; 14103 C; 14728 G; 20634 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 8; Length 68230;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
||||| |||| |||||||||||||||||||| ||||||||||||||||
Db 66085 GAGGAGGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAG 66038

RESULT 12
ADA03065/c
ID ADA03065 standard; DNA; 68233 BP.
XX
AC ADA03065;
XX
DT 06-NOV-2003 (first entry)
XX
DE Mouse Ppp3cc carcinoma associated gene, SEQ ID NO:1583.
XX
KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
KW gene; ds.
XX
OS Mus sp.
XX
PN WO2003057146-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041414.
XX
PR 26-DEC-2001; 2001US-00035832.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX

DR WPI; 2003-587068/55.
XX
PT New recombinant nucleic acid encoding carcinoma associated protein,
PT useful for preparing compositions for treating carcinomas.
XX
PS Claim 1; SEQ ID NO 1583; 245pp; English.
XX
CC The invention relates to recombinant carcinoma associated (CA) nucleic
CC acid sequences from mouse and human (ADA01482-ADA03094), and to
CC recombinant carcinoma associated proteins (CAP) encoded by them. The
CC invention also encompasses expression vectors and host cells comprising a
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC binds to the protein, and a biochip comprising CA nucleic acid or
CC fragments thereof. The sequences of the invention were identified using
CC oncogenic retroviruses, which insert into the genome of the host organism
CC at random. Many of these do not carry transduced host oncogenes or
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC direct consequence of the effects of proviral integration into host
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC leukaemia) or a propensity to carcinoma by determination of the sequence
CC of a CA gene, or by determination of CA gene expression in particular
CC tissues. CA nucleic acids, proteins and antibodies are also useful as
CC therapeutic agents and in screening and evaluating drug candidates. The
CC present sequence represents a specifically claimed murine CA nucleic acid
CC sequence of the invention. Note: The complete sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;

```
  Query Match             81.6%;  Score 41.6;  DB 8;  Length 68233;
  Best Local Similarity   91.7%;  Pred. No. 0.12;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||| |||||||||||||||||||||||||||||| || |||
Db      66088 GAGGAGGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAG 66041
```

RESULT 13
ADB72803/c
ID ADB72803 standard; DNA; 68233 BP.
XX
AC ADB72803;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse Ppp3cc gene.
XX
KW mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
OS Mus sp.
XX
PN WO2003008583-A2.
XX
PD 30-JAN-2003.
XX
PF 26-DEC-2001; 2001WO-US051291.
XX
PR 02-MAR-2001; 2001US-00798586.
PR 23-OCT-2001; 2001US-00004113.
PR 08-NOV-2001; 2001US-00052482.
PR 30-NOV-2001; 2001US-00997722.
PR 20-DEC-2001; 2001US-00034650.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW, Engelhard EK;
XX
DR WPI; 2003-239337/23.
XX
PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
PT cancers, neoplasm, adenocarcinoma, or sarcomas.
XX
PS Claim 1; SEQ ID NO 631; 2304pp; English.
XX
CC The invention relates to a novel recombinant nucleic acid comprising a
CC nucleotide sequence selected from any of the 660 sequences fully defined
CC in the specification. A polynucleotide of the invention has cytostatic
CC activity, and may have a use in gene therapy, or in a vaccine. The
CC recombinant nucleic acids and polypeptides are useful for treating
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC sarcomas. The present sequence represents a mouse gene of the invention.
XX
SQ Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;

```
  Query Match             81.6%;  Score 41.6;  DB 9;  Length 68233;
  Best Local Similarity   91.7%;  Pred. No. 0.12;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||| |||||||||||||||||||||||||||||| || |||
Db      66088 GAGGAGGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAG 66041
```

RESULT 14
AAL38337/c
ID AAL38337 standard; DNA; 215980 BP.
XX
AC AAL38337;
XX
DT 15-AUG-2002 (first entry)
XX
DE Complementary strand of a genomic sequence encoding a mouse NgR3.
XX
KW Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue;
KW NgR2; NgR3; axonal growth; central nervous system; CNS; cerebral injury;
KW spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
KW monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
KW multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;
KW Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
KW Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;
KW transgenic animal; unregulated cellular growth; cancer; tumour; mouse;
KW murine; ds.
XX
OS Mus sp.
XX
PN WO200229059-A2.
XX
PD 11-APR-2002.
XX
PF 06-OCT-2001; 2001WO-US031488.
XX
PR 06-OCT-2000; 2000US-0238361P.
XX
PA (UYYA) UNIV YALE.
PA (BIOJ) BIOGEN INC.
XX
PI Strittmatter SM, Cate RL, Sah DWY;
XX
DR WPI; 2002-416677/44.
XX
PT Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for
PT treating central nervous system disorder, cerebral injury, spinal cord
PT injury, stroke, and demyelinating diseases.
XX
PS Example 16; Page 219-275; 277pp; English.
XX
CC The invention relates to a Nogo receptor homologue polypeptide, NgR2 or
CC NgR3, comprising a 50 amino acid LRRCT sequence, a 284 amino acid NTLRRCT
CC sequence, or a 420, 461 or 392 amino acid sequence, all given in the
CC specification. The NgR3 protein or its binding antibody is useful for
CC decreasing inhibition of axonal growth of a central nervous system (CNS)

CC neuron, by contacting the neuron NgR3 or its antibody, and for treating
CC CNS disease, disorder or injury. NgR3 or a vector comprising NgR3 is
CC useful for treating cerebral injury, spinal cord injury, stroke,
CC demyelinating diseases, e.g. multiple sclerosis, monophasic
CC demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC panencephalitis, Marchiafava-Bignami disease, Spongy degeneration,
CC Alexander's disease, Canavan's disease, metachromatic leukodystrophy and
CC Krabbe's disease. NgR3 is useful for inducing an immune response in a
CC mammal against NgR3, as a bait protein in a two-hybrid or three-hybrid
CC assay, and as a research tool for identification, characterisation and
CC purification of interacting, regulatory proteins. The nucleotide
CC sequences of the invention are useful for screening for RFLP associated
CC with certain disorders, for genetic mapping, and for gene therapy. The
CC vector containing NgR3 is useful for producing non-human transgenic
CC animals. The NgR3 binding antibody is useful for isolating and purifying
CC NgR3, for localisation and/or quantitation of NgR3, and for diagnostic
CC and therapeutic purposes. The sequences of the invention, vectors and
CC antibodies are useful for treating or preventing unregulated cellular
CC growth such as cancer and tumour growth. This polynucleotide sequence
CC represents the
XX
SQ Sequence 215980 BP; 56872 A; 50995 C; 50240 G; 54437 T; 0 U; 3436 Other;

Query Match 81.6%; Score 41.6; DB 6; Length 215980;
Best Local Similarity 91.7%; Pred. No. 0.13;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  ||||||||||||||||||||||||||||||||||||
Db      19661 GAGGAGGAGGAAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 19614
```

RESULT 15
ABQ76418/c
ID ABQ76418 standard; cDNA; 1721 BP.
XX
AC ABQ76418;
XX
DT 21-NOV-2002 (first entry)
XX
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 261.
XX
KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
KW vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KW apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KW neurodegeneration; cell death; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200264766-A2.
XX
PD 22-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-EP015398.
XX
PR 22-DEC-2000; 2000EP-00870318.
PR 04-JAN-2001; 2001EP-00870002.
PR 09-JAN-2001; 2001EP-00870003.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX
DR WPI; 2002-667002/71.
DR P-PSDB; ABG93152.
XX
PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medicament for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
PS Claim 36; Fig 1; 344pp; English.
XX

CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide; immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides , or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention
XX
SQ Sequence 1721 BP; 501 A; 400 C; 341 G; 479 T; 0 U; 0 Other;

Query Match 79.6%; Score 40.6; DB 6; Length 1721;
Best Local Similarity 91.5%; Pred. No. 0.2;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              || |||||||  |||||||||||| |||||||||||||||||||||||
Db        631 GAAGATGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGA 585
```

Search completed: March 2, 2004, 05:39:00
Job time : 267.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:39:14 ; Search time 60 Seconds
(without alignments)
471.708 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	2072	4	US-09-016-434-1181	Sequence 1181, Ap
	2	40	78.4	2663	4	US-09-533-029-47	Sequence 47, Appl
	3	38.4	75.3	636	4	US-09-702-705-1668	Sequence 1668, Ap
	4	38.4	75.3	636	4	US-09-736-457-1668	Sequence 1668, Ap
	5	38.4	75.3	636	4	US-09-614-124B-1668	Sequence 1668, Ap
	6	38.4	75.3	636	4	US-09-671-325-1668	Sequence 1668, Ap
	7	38.4	75.3	650	3	US-09-328-111-333	Sequence 333, App
	8	37.4	73.3	1194	4	US-09-220-132-31	Sequence 31, Appl
	9	36.8	72.2	58	3	US-08-860-038-15	Sequence 15, Appl
c	10	36.8	72.2	58	3	US-08-860-038-16	Sequence 16, Appl
	11	36.8	72.2	58	4	US-09-580-923-15	Sequence 15, Appl
c	12	36.8	72.2	58	4	US-09-580-923-16	Sequence 16, Appl
c	13	36.8	72.2	661	4	US-09-894-998A-34	Sequence 34, Appl
	14	36.8	72.2	744	3	US-09-163-285-3	Sequence 3, Appli
	15	36.8	72.2	1512	3	US-09-163-285-1	Sequence 1, Appli
	16	36.8	72.2	1633	4	US-09-702-705-316	Sequence 316, App
	17	36.8	72.2	1633	4	US-09-702-705-788	Sequence 788, App
	18	36.8	72.2	1633	4	US-09-736-457-316	Sequence 316, App
	19	36.8	72.2	1633	4	US-09-736-457-788	Sequence 788, App
	20	36.8	72.2	1633	4	US-09-614-124B-316	Sequence 316, App
	21	36.8	72.2	1633	4	US-09-614-124B-788	Sequence 788, App
	22	36.8	72.2	1633	4	US-09-671-325-316	Sequence 316, App
	23	36.8	72.2	1633	4	US-09-671-325-788	Sequence 788, App
	24	36.8	72.2	1633	4	US-09-589-184-316	Sequence 316, App
	25	36.8	72.2	1633	4	US-09-589-184-788	Sequence 788, App
	26	36.8	72.2	2817	4	US-09-620-312D-1085	Sequence 1085, Ap
	27	36.8	72.2	5561	4	US-09-418-710-28	Sequence 28, Appl
	28	36.8	72.2	5573	4	US-09-418-710-30	Sequence 30, Appl
	29	36.8	72.2	6114	4	US-09-495-714C-5	Sequence 5, Appli
	30	36.8	72.2	43676	3	US-09-356-952-12	Sequence 12, Appl
c	31	36.8	72.2	51259	3	US-08-781-891-209	Sequence 209, App
c	32	36.8	72.2	51259	4	US-09-618-166-209	Sequence 209, App
	33	36.4	71.4	2609	3	US-09-141-212-7	Sequence 7, Appli
	34	36.4	71.4	2609	3	US-09-561-138-7	Sequence 7, Appli
	35	36.4	71.4	2669	3	US-09-141-212-9	Sequence 9, Appli
	36	36.4	71.4	2669	3	US-09-561-138-9	Sequence 9, Appli
	37	36.4	71.4	2693	3	US-09-141-212-5	Sequence 5, Appli
	38	36.4	71.4	2693	3	US-09-561-138-5	Sequence 5, Appli
	39	36.4	71.4	3255	2	US-08-916-917-11	Sequence 11, Appl
	40	36.4	71.4	3255	3	US-09-225-170-11	Sequence 11, Appl
	41	36.4	71.4	3630	3	US-09-378-255-5	Sequence 5, Appli
	42	36.4	71.4	3630	3	US-09-141-212-1	Sequence 1, Appli
	43	36.4	71.4	3630	3	US-09-141-212-3	Sequence 3, Appli
	44	36.4	71.4	3630	3	US-09-552-351-3	Sequence 3, Appli
	45	36.4	71.4	3630	3	US-09-251-372-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178197
US-09-016-434-1181

Query Match 100.0%; Score 51; DB 4; Length 2072;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGT 1342
```

RESULT 2
US-09-533-029-47
; Sequence 47, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 2663
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1089
US-09-533-029-47

Query Match 78.4%; Score 40; DB 4; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.019;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || || |||| ||| ||||||||||||||||| ||||||||||||||||
Db        865 GATGACGAAGATGAGGAGGAGGAAGAGGAGGAAGAGGAGGAGGAAGAG 912
```

RESULT 3
US-09-702-705-1668
; Sequence 1668, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || ||||||| || |||||||||||| |||||||||||||||||| |||
Db        571 GAAGATGAAGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAG 618
```

RESULT 4
US-09-736-457-1668
; Sequence 1668, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || ||||||| || |||||||||||| |||||||||||||||||| |||
Db        571 GAAGATGAAGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAG 618
```

RESULT 5
US-09-614-124B-1668
; Sequence 1668, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA

```
;   ORGANISM: Homo sapiens
US-09-614-124B-1668

  Query Match             75.3%;  Score 38.4;  DB 4;  Length 636;
  Best Local Similarity   87.5%;  Pred. No. 0.045;
  Matches   42;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || |||||||  || ||||||||||| ||||||||||||||||| |||
Db        571 GAAGATGAAGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAG 618


RESULT 6
US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C12
;  CURRENT APPLICATION NUMBER: US/09/671,325
;  CURRENT FILING DATE:  2000-09-26
;  NUMBER OF SEQ ID NOS:  1825
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-671-325-1668

  Query Match             75.3%;  Score 38.4;  DB 4;  Length 636;
  Best Local Similarity   87.5%;  Pred. No. 0.045;
  Matches   42;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || |||||||  || ||||||||||| ||||||||||||||||| |||
Db        571 GAAGATGAAGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAG 618


RESULT 7
US-09-328-111-333
; Sequence 333, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(650)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-333

  Query Match             75.3%;  Score 38.4;  DB 3;  Length 650;
  Best Local Similarity   87.5%;  Pred. No. 0.045;
  Matches   42;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||| |||||| ||| |||||||||||||| || |||||||||| |||
Db        230 GAGAATGAAGATGATGAGGAGGAAGAGGAAGAAGAGGAGGAGGAGGAG 277


RESULT 8
US-09-220-132-31
; Sequence 31, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
;  TITLE OF INVENTION:  OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCEF
;  FILE REFERENCE:  07334-074001
;  CURRENT APPLICATION NUMBER: US/09/220,132
;  CURRENT FILING DATE:  1998-12-23
;  PRIOR APPLICATION NUMBER:  US 60/079,303
;  PRIOR FILING DATE:  1998-03-25
;  PRIOR APPLICATION NUMBER:  US 60/068,821
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  191
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 1194
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-31

  Query Match             73.3%;  Score 37.4;  DB 4;  Length 1194;
  Best Local Similarity   87.2%;  Pred. No. 0.085;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| |||| ||| || || |||||||| ||||||||||||||||
Db        635 GAGGAGGAAGGTGAGGAAGATGAAGAGGATGAGGAGGAGGAGGAAGA 681


RESULT 9
US-08-860-038-15
; Sequence 15, Application US/08860038
; Patent No. 6287762
;  GENERAL INFORMATION:
;    APPLICANT:  CROUZET, Joel
;    APPLICANT:  SCHERMAN, Daniel
;    APPLICANT:  WILS, Pierre
;    TITLE OF INVENTION:  PURIFICATION OF A TRIPLE HELIX FORMATION
;    TITLE OF INVENTION:  WITH AN IMMOBILIZED OLIGONUCLEOTIDE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/860,038
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  FR 94/15162
;       FILING DATE:  16-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO FR95/01468
;       FILING DATE:  08-NOV-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Savitzky Esq., Martin F.
;       REGISTRATION NUMBER:  29,699
;       REFERENCE/DOCKET NUMBER:  ST94090-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (610) 454-3816
;       TELEFAX:  (610) 454-3808
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  58 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  other nucleic acid
;       DESCRIPTION:  /desc = "Oligonucleotide"
US-08-860-038-15

  Query Match             72.2%;  Score 36.8;  DB 3;  Length 58;
  Best Local Similarity   85.4%;  Pred. No. 0.099;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  || |||||||| ||||||||||||||||||||| |||
Db          7 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 54


RESULT 10
US-08-860-038-16/c
; Sequence 16, Application US/08860038
; Patent No. 6287762
;  GENERAL INFORMATION:
;    APPLICANT:  CROUZET, Joel
;    APPLICANT:  SCHERMAN, Daniel
;    APPLICANT:  WILS, Pierre
;    TITLE OF INVENTION:  PURIFICATION OF A TRIPLE HELIX FORMATION
;    TITLE OF INVENTION:  WITH AN IMMOBILIZED OLIGONUCLEOTIDE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, Mailstop 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/860,038
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 94/15162
;      FILING DATE:  16-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO FR95/01468
;      FILING DATE:  08-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savitzky Esq., Martin F.
;      REGISTRATION NUMBER:  29,699
;      REFERENCE/DOCKET NUMBER:  ST94090-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3816
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  58 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Oligonucleotide"
US-08-860-038-16

  Query Match             72.2%;  Score 36.8;  DB 3;  Length 58;
  Best Local Similarity   85.4%;  Pred. No. 0.099;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  || |||||||| ||||||||||||||||||||| |||
Db         56 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAG 9


RESULT 11
US-09-580-923-15
; Sequence 15, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
;  APPLICANT:  Crouzet, Joel
;  APPLICANT:  Scherman, Daniel
;  APPLICANT:  Wils, Pierre
;  APPLICANT:  Cameron, Beatrice
;  APPLICANT:  Blanche, Francis
;  TITLE OF INVENTION:  PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;  TITLE OF INVENTION:  IMMOBILIZED OLIGONUCLEOTIDE
;  FILE REFERENCE:  03804.0138-01
;  CURRENT APPLICATION NUMBER: US/09/580,923
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  08/860,038
;  PRIOR FILING DATE:  1997-06-09
;  PRIOR APPLICATION NUMBER:  PCT/FR95/01468
;  PRIOR FILING DATE:  1995-11-08
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 15
;    LENGTH: 58
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:
;    OTHER INFORMATION: oligonucleotide
US-09-580-923-15

  Query Match             72.2%;  Score 36.8;  DB 4;  Length 58;
  Best Local Similarity   85.4%;  Pred. No. 0.099;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  || |||||||| ||||||||||||||||||||| |||
Db          7 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAG 54


RESULT 12
US-09-580-923-16/c
; Sequence 16, Application US/09580923
; Patent No. 6319672
; GENERAL INFORMATION:
;  APPLICANT:  Crouzet, Joel
;  APPLICANT:  Scherman, Daniel
;  APPLICANT:  Wils, Pierre
;  APPLICANT:  Cameron, Beatrice
;  APPLICANT:  Blanche, Francis
```

```
;  TITLE OF INVENTION:  PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;  TITLE OF INVENTION:  IMMOBILIZED OLIGONUCLEOTIDE
;  FILE REFERENCE:  03804.0138-01
;  CURRENT APPLICATION NUMBER: US/09/580,923
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  08/860,038
;  PRIOR FILING DATE:  1997-06-09
;  PRIOR APPLICATION NUMBER:  PCT/FR95/01468
;  PRIOR FILING DATE:  1995-11-08
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 58
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: oligonucleotide
US-09-580-923-16

  Query Match             72.2%;  Score 36.8;  DB 4;  Length 58;
  Best Local Similarity   85.4%;  Pred. No. 0.099;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  || |||||||| |||||||||||||||||||| |||
Db         56 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAG 9


RESULT 13
US-09-894-998A-34/c
; Sequence 34, Application US/09894998A
; Patent No. 6537555
; GENERAL INFORMATION:
;  APPLICANT: Hosken, Nancy Ann
;  APPLICANT:  Craig H. Day
;  APPLICANT:  Davin C. Dillon
;  APPLICANT:  McGowan, Patrick
;  APPLICANT:  Sleath, Paul R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;  FILE REFERENCE: 210121.538
;  CURRENT APPLICATION NUMBER: US/09/894,998A
;  CURRENT FILING DATE:  2001-06-28
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 661
;   TYPE: DNA
;   ORGANISM: HSV-2
US-09-894-998A-34

  Query Match             72.2%;  Score 36.8;  DB 4;  Length 661;
  Best Local Similarity   85.4%;  Pred. No. 0.12;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  || |||| |||||||||||||||||||| |||||||
Db         51 GAGGAGGAGGAGGAGGAGGCGGAAGAGGAGGAGGAGGAGGCGGAAGAG 4


RESULT 14
US-09-163-285-3
; Sequence 3, Application US/09163285
; Patent No. 6204013
;  GENERAL INFORMATION:
;    APPLICANT:  Khodadoust, Mehran
;    TITLE OF INVENTION:  NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/090,398
;      FILING DATE:  June 24, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mandragouras, Amy E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  MNI-049
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)742-4214
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  744 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..744
US-09-163-285-3

  Query Match             72.2%;  Score 36.8;  DB 3;  Length 744;
  Best Local Similarity   85.4%;  Pred. No. 0.12;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || ||  || | |||| |||||||||| ||||||||||||||||||||
Db        628 GAAGAGAAAACAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAG 675


RESULT 15
US-09-163-285-1
; Sequence 1, Application US/09163285
; Patent No. 6204013
;  GENERAL INFORMATION:
;    APPLICANT:  Khodadoust, Mehran
;    TITLE OF INVENTION:  NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD, LLP
;      STREET:  28 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,285
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/090,398
;      FILING DATE:  June 24, 1998
;    ATTORNEY/AGENT INFORMATION:
```

; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 125..868
US-09-163-285-1

Query Match 72.2%; Score 36.8; DB 3; Length 1512;
Best Local Similarity 85.4%; Pred. No. 0.12;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || ||  || | |||| |||||||||| ||||||||||||||||||||
Db        752 GAAGAGAAAACAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAG 799
```

Search completed: March 2, 2004, 08:36:49
Job time : 61 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 10:12:50 ; Search time 140 Seconds
(without alignments)
1314.149 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		51	100.0	1353	9	US-09-825-923-3	Sequence 3, Appli
2		51	100.0	1353	14	US-10-077-870-3	Sequence 3, Appli
3		51	100.0	1353	14	US-10-001-073-1	Sequence 1, Appli
4		51	100.0	2072	15	US-10-305-720-1181	Sequence 1181, Ap
5		51	100.0	3274	14	US-10-225-567A-41	Sequence 41, Appl
6	c	41.6	81.6	68233	15	US-10-034-650-31	Sequence 31, Appl
7	c	41.6	81.6	215980	10	US-09-972-546-16	Sequence 16, Appl
8		40.2	78.8	1344	9	US-09-825-923-1	Sequence 1, Appli
9		40.2	78.8	1344	14	US-10-077-870-1	Sequence 1, Appli
10		40	78.4	223	9	US-09-728-444-146	Sequence 146, App
11	c	40	78.4	234	9	US-09-728-446-1420	Sequence 1420, Ap
12		40	78.4	330	9	US-09-728-444-124	Sequence 124, App
13		40	78.4	642	12	US-10-425-114-10213	Sequence 10213, A
14		40	78.4	1173	15	US-10-161-927-81	Sequence 81, Appl
15		40	78.4	1178	15	US-10-161-927-83	Sequence 83, Appl
16		40	78.4	1290	12	US-10-424-599-47976	Sequence 47976, A
17		40	78.4	1433	12	US-10-425-114-19415	Sequence 19415, A
18		40	78.4	2367	14	US-10-128-714-6204	Sequence 6204, Ap
19		40	78.4	2367	14	US-10-128-714-7204	Sequence 7204, Ap
20		40	78.4	2663	10	US-09-533-029-47	Sequence 47, Appl
21		40	78.4	2663	10	US-09-934-455-177	Sequence 177, App
22		40	78.4	2663	15	US-10-225-068-65	Sequence 65, Appl
23		40	78.4	2663	15	US-10-302-267-45	Sequence 45, Appl
24		40	78.4	2663	15	US-10-374-780A-229	Sequence 229, App
25		40	78.4	4238	14	US-10-128-714-204	Sequence 204, App
26		40	78.4	4367	14	US-10-128-714-5204	Sequence 5204, Ap
27	c	39	76.5	191	14	US-10-029-386-17979	Sequence 17979, A
28		39	76.5	423	9	US-09-864-761-18355	Sequence 18355, A
29		39	76.5	487	9	US-09-864-761-1597	Sequence 1597, Ap
30	c	39	76.5	543	14	US-10-029-386-4279	Sequence 4279, Ap
31		39	76.5	1764	16	US-10-211-859-4	Sequence 4, Appli
32		39	76.5	1788	10	US-09-893-519A-115	Sequence 115, App
33		39	76.5	1977	14	US-10-102-806-216	Sequence 216, App
34	c	39	76.5	2134	15	US-10-027-632-97636	Sequence 97636, A
35		39	76.5	2480	15	US-10-027-632-103743	Sequence 103743,
36		39	76.5	2480	15	US-10-027-632-111750	Sequence 111750,
37	c	39	76.5	3769	14	US-10-175-523-184	Sequence 184, App
38		39	76.5	23130	9	US-09-764-869-1892	Sequence 1892, Ap
39		39	76.5	23130	14	US-10-091-504-1892	Sequence 1892, Ap
40		39	76.5	23130	15	US-10-227-577-1892	Sequence 1892, Ap
41	c	39	76.5	53226	9	US-09-818-264-3	Sequence 3, Appli
42	c	39	76.5	106664	14	US-10-175-523-97	Sequence 97, Appl
43	c	38.6	75.7	6222	15	US-10-120-988-114	Sequence 114, App
44	c	38.6	75.7	6452	9	US-09-954-456-308	Sequence 308, App
45		38.4	75.3	54	15	US-10-418-182-296	Sequence 296, App

ALIGNMENTS

RESULT 1
US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
US-09-825-923-3

Query Match 100.0%; Score 51; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930
```

RESULT 2
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match 100.0%; Score 51; DB 14; Length 1353;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930
```

RESULT 3
US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query Match 100.0%; Score 51; DB 14; Length 1353;
Best Local Similarity 100.0%; Pred. No. 9.7e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930
```

RESULT 4
US-10-305-720-1181
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressior
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match 100.0%; Score 51; DB 15; Length 2072;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 1342
```

RESULT 5
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 100.0%; Score 51; DB 14; Length 3274;
Best Local Similarity 100.0%; Pred. No. 9.4e-06;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930
```

RESULT 6
US-10-034-650-31/c
; Sequence 31, Application US/10034650
; Publication No. US20030216558A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000128
; CURRENT APPLICATION NUMBER: US/10/034,650

```
;  CURRENT FILING DATE:  2002-07-23
;  PRIOR APPLICATION NUMBER: US 09/474,377
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 68233
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-034-650-31

  Query Match             81.6%;  Score 41.6;  DB 15;  Length 68233;
  Best Local Similarity   91.7%;  Pred. No. 0.0037;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||| |||||||||||||||||||||||||||| || |||
Db      66088 GAGGAGGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGGAG 66041


RESULT 7
US-09-972-546-16/c
; Sequence 16, Application US/09972546
; Publication No. US20030124704A1
; GENERAL INFORMATION:
;  APPLICANT: STRITTMATTER, STEPHEN M.
;  APPLICANT:  CATE, RICHARD L.
;  APPLICANT:  SAH, DINAH W.Y.
;  TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
;  FILE REFERENCE: A116US
;  CURRENT APPLICATION NUMBER: US/09/972,546
;  CURRENT FILING DATE:  2001-10-06
;  PRIOR APPLICATION NUMBER: 60/238,361
;  PRIOR FILING DATE: 2000-10-06
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 215980
;   TYPE: DNA
;   ORGANISM: Mus sp.
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1001)..(1100)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (2123)..(2222)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (3728)..(3827)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (5168)..(5267)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (7481)..(7580)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (8849)..(8948)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (10375)..(10474)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (12270)..(12369)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (13438)..(13537)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (15902)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (15939)..(16038)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (18223)..(18322)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (20974)..(21073)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (24403)..(24502)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (27574)..(27673)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (30892)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (30901)..(31000)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (34443)..(34542)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (38205)..(38304)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (42373)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (42386)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (42393)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (42461)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (44809)..(44908)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (51380)..(51479)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (56740)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (56765)..(56864)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (62818)..(62917)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (68518)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (68534)..(68633)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (74552)..(74651)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (81446)..(81545)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (88519)..(88618)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
;   LOCATION: (93791)
;   OTHER INFORMATION: a, t, c, g, other or unknown
;   NAME/KEY: modified_base
```

; LOCATION: (93794)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96565)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96570)..(96573)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96579)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96590)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96596)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96602)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96616)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96629)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96633)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96668)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (96715)..(96814)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (104447)..(104546)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (114521)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (114527)..(114626)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (127063)..(127162)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (139133)..(139232)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (151051)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (153242)..(153341)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (164706)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (164708)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (164710)..(164809)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (182242)..(182341)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (192158)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (192192)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (198842)..(198941)
; OTHER INFORMATION: a, t, c, g, other or unknown
; NAME/KEY: modified_base

Query Match 81.6%; Score 41.6; DB 10; Length 215980;
Best Local Similarity 91.7%; Pred. No. 0.0035;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || | ||||||||||||||||||||||||||||||||||||
Db      19661 GAGGAGGAGGAAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 19614
```

RESULT 8
US-09-825-923-1
; Sequence 1, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

Query Match 78.8%; Score 40.2; DB 9; Length 1344;
Best Local Similarity 93.3%; Pred. No. 0.01;
Matches 42; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAA 45
              |||||||||||||||||||||||||||||||||||||||   |||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAA 924
```

RESULT 9
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21

```
;  PRIOR APPLICATION NUMBER: FI 20010323
;  PRIOR FILING DATE: 2001-02-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1341)
;   OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

  Query Match             78.8%;  Score 40.2;  DB 14;  Length 1344;
  Best Local Similarity   93.3%;  Pred. No. 0.01;
  Matches   42;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAA 45
              |||||||||||||||||||||||||||||||||||||||||   |||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAA 924


RESULT 10
US-09-728-444-146
; Sequence 146, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
;  APPLICANT: Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
;  TITLE OF INVENTION:  and Mutant Cells and Mutant Animals Defined Thereby
;  FILE REFERENCE: LEX-0100-USA
;  CURRENT APPLICATION NUMBER: US/09/728,444
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/168,360
;  PRIOR FILING DATE: 1999-12-01
;  NUMBER OF SEQ ID NOS: 1206
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146
;   LENGTH: 223
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(223)
;   OTHER INFORMATION: n = A,T,C or G
US-09-728-444-146

  Query Match             78.4%;  Score 40;  DB 9;  Length 223;
  Best Local Similarity   89.6%;  Pred. No. 0.013;
  Matches   43;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              |||||  ||||  ||||||||||| ||||||||||||||||||| |||
Db         14 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAG 61


RESULT 11
US-09-728-446-1420/c
; Sequence 1420, Application US/09728446
; Patent No. US20020081668A1
; GENERAL INFORMATION:
;  APPLICANT: Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020081668A1el Murine Polynucleotide Sequences
;  TITLE OF INVENTION:  and Mutant Cells and Mutant Animals Defined Thereby
;  FILE REFERENCE: LEX-0101-USA
;  CURRENT APPLICATION NUMBER: US/09/728,446
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/168,270
;  PRIOR FILING DATE: 1999-12-01
;  NUMBER OF SEQ ID NOS: 1461
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1420
;   LENGTH: 234
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(234)
;   OTHER INFORMATION: n = A,T,C or G
US-09-728-446-1420

  Query Match             78.4%;  Score 40;  DB 9;  Length 234;
  Best Local Similarity   89.6%;  Pred. No. 0.013;
  Matches   43;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              |||||  ||||  |||||||||||||||||| ||||||||  |||||||||
Db        174 GAGGAGGAAGAGGAAGAGGAGGAAGAGGAAGAGGAGGAAGAGGAAGAG 127


RESULT 12
US-09-728-444-124
; Sequence 124, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
;  APPLICANT: Friedrich, Glenn
;  APPLICANT:  Zambrowicz, Brian
;  APPLICANT:  Sands, Arthur T.
;  TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
;  TITLE OF INVENTION:  and Mutant Cells and Mutant Animals Defined Thereby
;  FILE REFERENCE: LEX-0100-USA
;  CURRENT APPLICATION NUMBER: US/09/728,444
;  CURRENT FILING DATE:  2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/168,360
;  PRIOR FILING DATE: 1999-12-01
;  NUMBER OF SEQ ID NOS: 1206
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
;   LENGTH: 330
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(330)
;   OTHER INFORMATION: n = A,T,C or G
US-09-728-444-124

  Query Match             78.4%;  Score 40;  DB 9;  Length 330;
  Best Local Similarity   89.6%;  Pred. No. 0.013;
  Matches   43;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              |||||  ||||  ||||| |||||||||||||||||| ||||||||||
Db        113 GAGGAGGAAGAGGAAGAAGAGGAAGAGGAGGAGGAGAAGGAGGAAGAG 160


RESULT 13
US-10-425-114-10213
; Sequence 10213, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
```

Tue Mar 2 17:00:55 2004

```
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
;  SEQ ID NO 10213
;    LENGTH: 642
;    TYPE: DNA
;    ORGANISM: Glycine max
;    FEATURE:
;    OTHER INFORMATION: Clone ID: 700899387_FLI
US-10-425-114-10213

  Query Match           78.4%;  Score 40;  DB 12;  Length 642;
  Best Local Similarity 89.6%;  Pred. No. 0.012;
  Matches   43;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              ||||||| | ||| || ||||| ||||||||||||||||||||||
Db        231 GAGGATGAGGATGAGGATGAGGATGAGGAGGAGGAGGAGGAAGAG 278


RESULT 14
US-10-161-927-81
;  Sequence 81, Application US/10161927
;  Publication No. US20030235821A1
;  GENERAL INFORMATION:
;    APPLICANT: Zerhusen, Bryan D.
;    APPLICANT:  Kekuda, Ramesh
;    APPLICANT:  Spytek, Kimberly A.
;    APPLICANT:  Shenoy, Suresh G.
;    APPLICANT:  Miller, Charles E.
;    APPLICANT:  Hjalt, Tord
;    APPLICANT:  Gerlach, Valerie L.
;    APPLICANT:  Baumgartner, Jason C.
;    APPLICANT:  Guo, Xiaojia
;    APPLICANT:  Gangolli, Esha A.
;    APPLICANT:  Vernet, Corine
;    APPLICANT:  Padigaru, Muralidhara
;    APPLICANT:  Li, Li
;    APPLICANT:  Pena, Carol E.A.
;    APPLICANT:  Gorman, Linda
;    APPLICANT:  Anderson, David W.
;    APPLICANT:  Edinger, Shlomit R.
;    APPLICANT:  Patturajan, Meera
;    APPLICANT:  Stone, David J.
;    TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS .C
;    TITLE OF INVENTION:  THE SAME
;    FILE REFERENCE: 21402-377 D (Cura 677 Other)
;    CURRENT APPLICATION NUMBER: US/10/161,927
;    CURRENT FILING DATE:  2002-06-03
;    PRIOR APPLICATION NUMBER: 60/295,661
;    PRIOR FILING DATE: 2001-06-04
;    PRIOR APPLICATION NUMBER: 60/295,607
;    PRIOR FILING DATE: 2001-06-04
;    PRIOR APPLICATION NUMBER: 60/296,404
;    PRIOR FILING DATE: 2001-06-06
;    PRIOR APPLICATION NUMBER: 60/296,418
;    PRIOR FILING DATE: 2001-06-06
;    PRIOR APPLICATION NUMBER: 60/296,575
;    PRIOR FILING DATE: 2001-06-07
;    PRIOR APPLICATION NUMBER: 60/297,414
;    PRIOR FILING DATE: 2001-06-11
;    PRIOR APPLICATION NUMBER: 60/297,567
;    PRIOR FILING DATE: 2001-06-12
;    PRIOR APPLICATION NUMBER: 60/298,528
;    PRIOR FILING DATE: 2001-06-15
;    PRIOR APPLICATION NUMBER: 60/325,685
;    PRIOR FILING DATE: 2001-09-27
;    PRIOR APPLICATION NUMBER: 60/299,133
;    PRIOR FILING DATE: 2001-06-18
;    Remaining Prior Application data removed - See File Wrapper or PALM.
;    NUMBER OF SEQ ID NOS: 190
;  SEQ ID NO 81
;    LENGTH: 1173
;    TYPE  DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (26)..(1166)
;
US-10-161-927-81

  Query Match           78.4%;  Score 40;  DB 15;  Length 1173;
  Best Local Similarity 89.6%;  Pred. No. 0.012;
  Matches   43;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  ||||||||||||||||| ||||||||||||||||
Db        512 GAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGAGGAGGAGGAGGAAGAG 559


RESULT 15
US-10-161-927-83
;  Sequence 83, Application US/10161927
;  Publication No. US20030235821A1
;  GENERAL INFORMATION:
;    APPLICANT: Zerhusen, Bryan D.
;    APPLICANT:  Kekuda, Ramesh
;    APPLICANT:  Spytek, Kimberly A.
;    APPLICANT:  Shenoy, Suresh G.
;    APPLICANT:  Miller, Charles E.
;    APPLICANT:  Hjalt, Tord
;    APPLICANT:  Gerlach, Valerie L.
;    APPLICANT:  Baumgartner, Jason C.
;    APPLICANT:  Guo, Xiaojia
;    APPLICANT:  Gangolli, Esha A.
;    APPLICANT:  Vernet, Corine
;    APPLICANT:  Padigaru, Muralidhara
;    APPLICANT:  Li, Li
;    APPLICANT:  Pena, Carol E.A.
;    APPLICANT:  Gorman, Linda
;    APPLICANT:  Anderson, David W.
;    APPLICANT:  Edinger, Shlomit R.
;    APPLICANT:  Patturajan, Meera
;    APPLICANT:  Stone, David J.
;    TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
;    TITLE OF INVENTION:  THE SAME
;    FILE REFERENCE: 21402-377 D (Cura 677 Other)
;    CURRENT APPLICATION NUMBER: US/10/161,927
;    CURRENT FILING DATE:  2002-06-03
;    PRIOR APPLICATION NUMBER: 60/295,661
;    PRIOR FILING DATE: 2001-06-04
;    PRIOR APPLICATION NUMBER: 60/295,607
;    PRIOR FILING DATE: 2001-06-04
;    PRIOR APPLICATION NUMBER: 60/296,404
;    PRIOR FILING DATE: 2001-06-06
;    PRIOR APPLICATION NUMBER: 60/296,418
;    PRIOR FILING DATE: 2001-06-06
;    PRIOR APPLICATION NUMBER: 60/296,575
;    PRIOR FILING DATE: 2001-06-07
;    PRIOR APPLICATION NUMBER: 60/297,414
;    PRIOR FILING DATE: 2001-06-11
;    PRIOR APPLICATION NUMBER: 60/297,567
;    PRIOR FILING DATE: 2001-06-12
;    PRIOR APPLICATION NUMBER: 60/298,528
;    PRIOR FILING DATE: 2001-06-15
;    PRIOR APPLICATION NUMBER: 60/325,685
;    PRIOR FILING DATE: 2001-09-27
;    PRIOR APPLICATION NUMBER: 60/299,133
;    PRIOR FILING DATE: 2001-06-18
;    Remaining Prior Application data removed - See File Wrapper or PALM.
;    NUMBER OF SEQ ID NOS: 190
;  SEQ ID NO 83
;    LENGTH: 1178
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(1141)
```

US-10-161-927-83

Query Match 78.4%; Score 40; DB 15; Length 1178;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || |  |||||||||||||||| ||||||||||||||||||
Db        487 GAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGAGGAGGAGGAGGAAGAG 534
```

Search completed: March 2, 2004, 12:03:38
Job time : 142 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 07:20:29 ; Search time 2886 Seconds
(without alignments)
621.792 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US098D_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US099E_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US099F_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US104A_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US104B_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US106_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US107A_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US107B_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6023A_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6023B_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
93: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*
94: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*
95: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*
96: /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
97: /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*
98: /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*
99: /cgn2_6/ptodata/2/pna/US6042_COMB.seq:*
100: /cgn2_6/ptodata/2/pna/US6043_COMB.seq:*
101: /cgn2_6/ptodata/2/pna/US6044_COMB.seq:*
102: /cgn2_6/ptodata/2/pna/US6045_COMB.seq:*
103: /cgn2_6/ptodata/2/pna/US6046_COMB.seq:*
104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:*
105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:*
106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:*
107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:*
109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:*
110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	69	29	US-09-692-077D-24	Sequence 24, Appl
2	51	100.0	69	43	US-10-001-073A-54	Sequence 54, Appl
c 3	51	100.0	481	72	US-60-164-763-274	Sequence 274, App
c 4	51	100.0	481	72	US-60-169-842-1935	Sequence 1935, Ap
c 5	51	100.0	481	73	US-60-170-346-61	Sequence 61, Appl
6	51	100.0	516	31	US-09-726-174-3537	Sequence 3537, Ap
7	51	100.0	569	72	US-60-160-189-1492	Sequence 1492, Ap
8	51	100.0	569	72	US-60-160-190-231	Sequence 231, App
9	51	100.0	569	72	US-60-160-202-659	Sequence 659, App
10	51	100.0	569	72	US-60-169-840-3708	Sequence 3708, Ap
11	51	100.0	569	72	US-60-169-841-1172	Sequence 1172, Ap
12	51	100.0	569	72	US-60-169-842-2193	Sequence 2193, Ap
13	51	100.0	569	72	US-60-169-867-3351	Sequence 3351, Ap
14	51	100.0	1353	20	US-09-422-985-3	Sequence 3, Appli
15	51	100.0	1353	29	US-09-692-077B-1	Sequence 1, Appli
16	51	100.0	1353	29	US-09-692-077D-1	Sequence 1, Appli
17	51	100.0	1353	33	US-09-825-923-3	Sequence 3, Appli
18	51	100.0	1353	43	US-10-001-073-1	Sequence 1, Appli
19	51	100.0	1353	43	US-10-001-073A-1	Sequence 1, Appli
20	51	100.0	1353	44	US-10-077-870-3	Sequence 3, Appli
21	51	100.0	1353	46	US-10-170-235-40719	Sequence 40719, A
22	51	100.0	1353	102	US-60-453-050-6437	Sequence 6437, Ap
23	51	100.0	1353	102	US-60-453-135-6437	Sequence 6437, Ap
24	51	100.0	1353	103	US-60-466-412-6437	Sequence 6437, Ap
25	51	100.0	1825	39	US-09-949-004-175	Sequence 175, App
26	51	100.0	2072	49	US-10-305-720-1181	Sequence 1181, Ap
27	51	100.0	3274	47	US-10-225-567A-41	Sequence 41, Appl
28	51	100.0	3655	107	US-60-500-315-890	Sequence 890, App
29	51	100.0	3891	107	US-60-500-315-891	Sequence 891, App
30	51	100.0	4050	76	US-60-207-360-68	Sequence 68, Appl
31	51	100.0	4050	76	US-60-207-360-110	Sequence 110, App
32	51	100.0	4050	76	US-60-207-360-111	Sequence 111, App
33	51	100.0	4050	76	US-60-207-360-112	Sequence 112, App
34	51	100.0	4050	76	US-60-207-360-113	Sequence 113, App
35	51	100.0	4050	76	US-60-207-360-114	Sequence 114, App
36	51	100.0	4050	76	US-60-207-360-115	Sequence 115, App
37	51	100.0	4050	76	US-60-207-360-116	Sequence 116, App
38	51	100.0	4050	76	US-60-207-360-117	Sequence 117, App
39	51	100.0	4050	76	US-60-207-360-118	Sequence 118, App
40	51	100.0	5259	78	US-60-229-515-121	Sequence 121, App
41	51	100.0	5349	81	US-60-245-225-211	Sequence 211, App
42	51	100.0	6786	81	US-60-248-505-165	Sequence 165, App
43	51	100.0	6806	39	US-09-949-004-641	Sequence 641, App
44	51	100.0	9842	73	US-60-172-373-2914	Sequence 2914, Ap
45	51	100.0	9842	89	US-60-324-185-27415	Sequence 27415, A

ALIGNMENTS

RESULT 1
US-09-692-077D-24
; Sequence 24, Application US/09692077D
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kersten M.
; TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-43
; CURRENT APPLICATION NUMBER: US/09/692,077D
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077D-24

Query Match 100.0%; Score 51; DB 29; Length 69;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 62
```

RESULT 2
US-10-001-073A-54
; Sequence 54, Application US/10001073A
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M.
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-42
; CURRENT APPLICATION NUMBER: US/10/001,073A
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073A-54

Query Match 100.0%; Score 51; DB 43; Length 69;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 62
```

RESULT 3
US-60-164-763-274/c
; Sequence 274, Application US/60164763
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
; FILE REFERENCE: CL000140
; CURRENT APPLICATION NUMBER: US/60/164,763
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 1154
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Human
US-60-164-763-274

Query Match 100.0%; Score 51; DB 72; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 177
```

RESULT 4
US-60-169-842-1935/c
; Sequence 1935, Application US/60169842
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
; FILE REFERENCE: CL000162
; CURRENT APPLICATION NUMBER: US/60/169,842
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 5232

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1935
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Human
US-60-169-842-1935

  Query Match             100.0%;  Score 51;  DB 72;  Length 481;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 177


RESULT 5
US-60-170-346-61/c
; Sequence 61, Application US/60170346
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
;  FILE REFERENCE: CL000147
;  CURRENT APPLICATION NUMBER: US/60/170,346
;  CURRENT FILING DATE: 1999-12-13
;  NUMBER OF SEQ ID NOS: 2600
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Human
US-60-170-346-61

  Query Match             100.0%;  Score 51;  DB 73;  Length 481;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 177


RESULT 6
US-09-726-174-3537
; Sequence 3537, Application US/09726174
; GENERAL INFORMATION:
;  APPLICANT:  Gearing, David P.
;  APPLICANT:  Holtzman, Douglas A.
;  TITLE OF INVENTION:  NOVEL NUCLEIC ACID MOLECULES AND USES
;  TITLE OF INVENTION:  THEREFOR
;  FILE REFERENCE:  1600.2012-001
;  CURRENT APPLICATION NUMBER: US/09/726,174
;  CURRENT FILING DATE:  2000-11-29
;  PRIOR APPLICATION NUMBER:  60/167,857
;  PRIOR FILING DATE:  1999-11-29
;  NUMBER OF SEQ ID NOS:  5942
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3537
;   LENGTH: 516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(516)
;   OTHER INFORMATION: n = A,T,C or G
US-09-726-174-3537

  Query Match             100.0%;  Score 51;  DB 31;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 293


RESULT 7
US-60-160-189-1492
; Sequence 1492, Application US/60160189
; GENERAL INFORMATION:
;  APPLICANT: BONAZZI, VIVIEN
;  TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000112
;  CURRENT APPLICATION NUMBER: US/60/160,189
;  CURRENT FILING DATE: 1999-10-19
;  NUMBER OF SEQ ID NOS: 10162
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1492
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-160-189-1492

  Query Match             100.0%;  Score 51;  DB 72;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74


RESULT 8
US-60-160-190-231
; Sequence 231, Application US/60160190
; GENERAL INFORMATION:
;  APPLICANT: BONAZZI, VIVIEN
;  TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: CL000115
;  CURRENT APPLICATION NUMBER: US/60/160,190
;  CURRENT FILING DATE: 1998-10-19
;  NUMBER OF SEQ ID NOS: 2384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 231
;   LENGTH: 569
;   TYPE: DNA
;   ORGANISM: HUMAN
US-60-160-190-231

  Query Match             100.0%;  Score 51;  DB 72;  Length 569;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74


RESULT 9
US-60-160-202-659
; Sequence 659, Application US/60160202
; GENERAL INFORMATION:
;  APPLICANT: BONAZZI, VIVIEN
;  TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
;  FILE REFERENCE: CL000114
;  CURRENT APPLICATION NUMBER: US/60/160,202
;  CURRENT FILING DATE: 1999-10-19
;  NUMBER OF SEQ ID NOS: 4392
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 659
```

; LENGTH: 569
; TYPE: DNA
; ORGANISM: HUMAN
US-60-160-202-659

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74

RESULT 10
US-60-169-840-3708
; Sequence 3708, Application US/60169840
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000164
; CURRENT APPLICATION NUMBER: US/60/169,840
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 9628
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3708
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Human
US-60-169-840-3708

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74

RESULT 11
US-60-169-841-1172
; Sequence 1172, Application US/60169841
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000163
; CURRENT APPLICATION NUMBER: US/60/169,841
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 2910
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1172
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Human
US-60-169-841-1172

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74

RESULT 12
US-60-169-842-2193
; Sequence 2193, Application US/60169842
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
; FILE REFERENCE: CL000162
; CURRENT APPLICATION NUMBER: US/60/169,842
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 5232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2193
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Human
US-60-169-842-2193

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74

RESULT 13
US-60-169-867-3351
; Sequence 3351, Application US/60169867
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000160
; CURRENT APPLICATION NUMBER: US/60/169,867
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 8230
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3351
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Human
US-60-169-867-3351

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 24 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 74

RESULT 14
US-09-422-985-3
; Sequence 3, Application US/09422985
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant

; CURRENT APPLICATION NUMBER: US/09/422,985
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
US-09-422-985-3

Query Match 100.0%; Score 51; DB 20; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930

RESULT 15
US-09-692-077B-1
; Sequence 1, Application US/09692077B
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
; FILE REFERENCE: Sequences 1-22
; CURRENT APPLICATION NUMBER: US/09/692,077B
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077B-1

Query Match 100.0%; Score 51; DB 29; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930

Search completed: March 2, 2004, 11:49:23
Job time : 2893 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 08:34:44 ; Search time 16.5 Seconds
(without alignments)
520.698 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 164199 seqs, 84230614 residues

Total number of hits satisfying chosen parameters: 328398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	40.6	79.6	1721	6	US-10-451-467A-261	Sequence 261, App
c 2	39	76.5	54303	6	US-10-417-375A-79	Sequence 79, Appl
c 3	38.8	76.1	150085	6	US-10-417-375A-167	Sequence 167, App
4	38.4	75.3	188053	6	US-10-417-375A-125	Sequence 125, App
5	37.4	73.3	3994	1	PCT-US04-02188-20	Sequence 20, Appl
6	37.4	73.3	3994	6	US-10-764-425-20	Sequence 20, Appl
7	37.4	73.3	45980	6	US-10-642-946-6	Sequence 6, Appli
8	37.4	73.3	398800	1	PCT-US03-32805-1	Sequence 1, Appli
9	37.2	72.9	310122	6	US-10-417-375A-1	Sequence 1, Appli
10	36.8	72.2	264	6	US-10-767-701-24209	Sequence 24209, A
11	36.8	72.2	34304	6	US-10-767-471-10555	Sequence 10555, A
12	36.8	72.2	54303	6	US-10-417-375A-79	Sequence 79, Appl
13	36.8	72.2	219715	6	US-10-417-375A-63	Sequence 63, Appl
c 14	35.8	70.2	650	6	US-10-767-701-26619	Sequence 26619, A
c 15	35.8	70.2	940	6	US-10-767-701-15708	Sequence 15708, A
16	35.8	70.2	1205	6	US-10-767-701-10125	Sequence 10125, A
c 17	35.8	70.2	2086	6	US-10-767-701-14827	Sequence 14827, A
c 18	35.6	69.8	1001	6	US-10-772-716-7	Sequence 7, Appli
19	35.2	69.0	1064	6	US-10-767-701-9500	Sequence 9500, Ap
c 20	35.2	69.0	310122	6	US-10-417-375A-1	Sequence 1, Appli
21	35	68.6	105077	6	US-10-417-375A-15	Sequence 15, Appl
22	34.6	67.8	666	6	US-10-767-701-23701	Sequence 23701, A
c 23	34.4	67.5	765267	6	US-10-767-471-10616	Sequence 10616, A
c 24	34.2	67.1	201	6	US-10-767-471-31476	Sequence 31476, A
c 25	34.2	67.1	962	6	US-10-451-467A-375	Sequence 375, App
26	34.2	67.1	1330	6	US-10-767-701-13517	Sequence 13517, A
27	34.2	67.1	1513	6	US-10-767-701-10140	Sequence 10140, A
c 28	34.2	67.1	803755	6	US-10-767-471-10700	Sequence 10700, A
29	33.8	66.3	2525	6	US-10-770-726-5	Sequence 5, Appli
c 30	33.8	66.3	46193	6	US-10-767-471-10632	Sequence 10632, A
c 31	33.6	65.9	201	6	US-10-767-471-39937	Sequence 39937, A
c 32	33.6	65.9	201	6	US-10-767-471-39939	Sequence 39939, A
c 33	33.6	65.9	201	6	US-10-767-471-39942	Sequence 39942, A
c 34	33.6	65.9	201	6	US-10-767-471-39944	Sequence 39944, A
c 35	33.6	65.9	707	6	US-10-767-701-11656	Sequence 11656, A
c 36	33.6	65.9	1316	6	US-10-767-701-13537	Sequence 13537, A
c 37	33.6	65.9	35895	6	US-10-767-471-10749	Sequence 10749, A
c 38	33.6	65.9	66158	6	US-10-765-790-72	Sequence 72, Appl
c 39	33.6	65.9	186191	6	US-10-767-471-10794	Sequence 10794, A
40	33.2	65.1	201	6	US-10-767-471-7934	Sequence 7934, Ap
41	33.2	65.1	201	6	US-10-767-471-7946	Sequence 7946, Ap
42	33.2	65.1	201	6	US-10-767-471-7957	Sequence 7957, Ap
43	33.2	65.1	201	6	US-10-767-471-30298	Sequence 30298, A
44	33.2	65.1	3129	6	US-10-767-471-423	Sequence 423, App
45	33.2	65.1	3253	6	US-10-767-471-422	Sequence 422, App

ALIGNMENTS

RESULT 1
US-10-451-467A-261/c
; Sequence 261, Application US/10451467A
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 261
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-261

Query Match 79.6%; Score 40.6; DB 6; Length 1721;
Best Local Similarity 91.5%; Pred. No. 0.0039;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              || |||||||  |||||||||| ||||||||||||||||||||||||
Db        631 GAAGATGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGA 585
```

RESULT 2
US-10-417-375A-79/c
; Sequence 79, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79

; LENGTH: 54303
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-417-375A-79

Query Match 76.5%; Score 39; DB 6; Length 54303;
Best Local Similarity 89.4%; Pred. No. 0.013;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
Db 51408 AGGAAGAAGAGAAGGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 51362

RESULT 3
US-10-417-375A-167/c
; Sequence 167, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 150085
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(150085)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-167

Query Match 76.1%; Score 38.8; DB 6; Length 150085;
Best Local Similarity 86.0%; Pred. No. 0.016;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTG 50
Db 54726 GAGGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAAGAGGG 54677

RESULT 4
US-10-417-375A-125
; Sequence 125, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 188053
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(188053)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-125

Query Match 75.3%; Score 38.4; DB 6; Length 188053;
Best Local Similarity 87.5%; Pred. No. 0.02;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
Db 63527 GAGGAGGAAGAAGAAGAGGAAGAAGAGGAGGAGGAGGAGGGGGAGGAG 63574

RESULT 5
PCT-US04-02188-20
; Sequence 20, Application PC/TUS0402188
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 3994
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-02188-20

Query Match 73.3%; Score 37.4; DB 1; Length 3994;
Best Local Similarity 87.2%; Pred. No. 0.028;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
Db 926 GAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAAGAGGAAGAAGA 972

RESULT 6
US-10-764-425-20
; Sequence 20, Application US/10764425
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 3994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-425-20

Query Match 73.3%; Score 37.4; DB 6; Length 3994;
Best Local Similarity 87.2%; Pred. No. 0.028;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
Db 926 GAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAAGAGGAAGAAGA 972

RESULT 7
US-10-642-946-6
; Sequence 6, Application US/10642946
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: Genomic Polynucleotide Fragments From Chromosome 7
; FILE REFERENCE: JR-14,000-US
; CURRENT APPLICATION NUMBER: US/10/642,946

```
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/957,956
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 60/234,422
;  PRIOR FILING DATE: 2001-09-21
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 45980
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-642-946-6

  Query Match            73.3%;  Score 37.4;  DB 6;  Length 45980;
  Best Local Similarity   87.2%;  Pred. No. 0.033;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| |||| ||||||||| || ||||| ||||||||||||||||||
Db       3845 GAGGAAGAAGAAGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAAGA 3891


RESULT 8
PCT-US03-32805-1
; Sequence 1, Application PC/TUS0332805
; GENERAL INFORMATION:
;  APPLICANT: deCODE genetics ehf.
;  APPLICANT:  Helgadottir, Anna
;  APPLICANT:  Gulcher, Jeffrey R.
;  APPLICANT:  Manolescu, Andrei
;  TITLE OF INVENTION: Susceptibility Gene for Myocardial
;  TITLE OF INVENTION:  Infarction
;  FILE REFERENCE: 2345.2048002
;  CURRENT APPLICATION NUMBER: PCT/US03/32805
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/419,432
;  PRIOR FILING DATE: 2002-10-17
;  NUMBER OF SEQ ID NOS: 535
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 398800
;   TYPE: DNA
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (70677)...(70776)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (154988)...(155087)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 248521
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (269991)...(270091)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (272544)...(272643)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (279545)...(279644)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (300892)...(300991)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (327555)...(327654)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (332849)...(332948)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (341698)...(341698)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (345190)...(345289)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (350504)...(350603)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (391524)...(391623)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (396625)...(396724)
;   OTHER INFORMATION: n = A,T, C or G
PCT-US03-32805-1

  Query Match            73.3%;  Score 37.4;  DB 1;  Length 398800;
  Best Local Similarity   87.2%;  Pred. No. 0.038;
  Matches   41;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| |||| ||| || || |||||||| ||||||||||||||||||
Db      51856 GAGGAGGAAGATGAGGAAGATGAAGAGGATGAGGAGGAGGAGGAAGA 51902


RESULT 9
US-10-417-375A-1
; Sequence 1, Application US/10417375A
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;  FILE REFERENCE: 529452001600
;  CURRENT APPLICATION NUMBER: US/10/417,375A
;  CURRENT FILING DATE:  2003-04-15
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 310122
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(310122)
;   OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-1

  Query Match            72.9%;  Score 37.2;  DB 6;  Length 310122;
  Best Local Similarity   84.0%;  Pred. No. 0.042;
  Matches   42;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTG 50
              || || ||||  |||||||||| |||||||||||||||||| || | |
Db     256497 GAAGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGGGGG 256546


RESULT 10
US-10-767-701-24209
; Sequence 24209, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
```

```
APPLICANT:  Zhou, Yihua
APPLICANT:  Cao, Yongwei
TITLE OF INVENTION:  Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE:  2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 24209
  LENGTH: 264
  TYPE: DNA
  ORGANISM: Sorghum bicolor
  FEATURE:
  OTHER INFORMATION: Clone ID: 30932345
US-10-767-701-24209

  Query Match             72.2%;  Score 36.8;  DB 6;  Length 264;
  Best Local Similarity   85.4%;  Pred. No. 0.032;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              ||||| |||| ||||||||||||||||||| || || |||||||||
Db        166 GAGGAGGAAGAAGAAGAGGAGGAAGAGGAAGAAGAAGAGGAGGAGGAG 213


RESULT 11
US-10-767-471-10555
; Sequence 10555, Application US/10767471
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001505
;  CURRENT APPLICATION NUMBER: US/10/767,471
;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 50231
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10555
;  LENGTH: 34304
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(34304)
;  OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10555

  Query Match             72.2%;  Score 36.8;  DB 6;  Length 34304;
  Best Local Similarity   85.4%;  Pred. No. 0.046;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              || || |||| |||| |||||| |||||||||||||||||| |||||||
Db       9950 GAAGAAGAAGAAGAGGGGAGGAGGAGGAGGAGGAGGAGGTGGAAGAG 9997


RESULT 12
US-10-417-375A-79
; Sequence 79, Application US/10417375A
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;  FILE REFERENCE: 529452001600
;  CURRENT APPLICATION NUMBER: US/10/417,375A
;  CURRENT FILING DATE:  2003-04-15
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
;  LENGTH: 54303
;  TYPE: DNA
;  ORGANISM  Mus musculus
US-10-417-375A-79

  Query Match             72.2%;  Score 36.8;  DB 6;  Length 54303;
  Best Local Similarity   85.4%;  Pred. No. 0.047;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || | |||||||||||||||||||| |||||||| || |||
Db        376 GAGGAAGAGGAGGAAGAGGAGGAAGAGGAAGAGGAGGAGGAAGAGGAG 423


RESULT 13
US-10-417-375A-63
; Sequence 63, Application US/10417375A
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;  FILE REFERENCE: 529452001600
;  CURRENT APPLICATION NUMBER: US/10/417,375A
;  CURRENT FILING DATE:  2003-04-15
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;  LENGTH: 219715
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(219715)
;  OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-63

  Query Match             72.2%;  Score 36.8;  DB 6;  Length 219715;
  Best Local Similarity   85.4%;  Pred. No. 0.052;
  Matches   41;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
              ||||| || | || |||||||| |||||||||||||||||||| |||
Db     107046 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 107093


RESULT 14
US-10-767-701-26619/c
; Sequence 26619, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 26619
;  LENGTH: 650
;  TYPE: DNA
;  ORGANISM: Sorghum bicolor
;  FEATURE:
;  OTHER INFORMATION: Clone ID: 30976844
US-10-767-701-26619

  Query Match             70.2%;  Score 35.8;  DB 6;  Length 650;
  Best Local Similarity   85.1%;  Pred. No. 0.063;
  Matches   40;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGA 47
              || || |||  |||||||| || ||||||||||||||||||| ||
Db         94 GACGACGAAGAAGAAGAGGAAGAGGAGGAGGAGGAGGAGGAGGA 48


RESULT 15
US-10-767-701-15708/c
```

; Sequence 15708, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 15708
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1381_2
US-10-767-701-15708

Query Match 70.2%; Score 35.8; DB 6; Length 940;
Best Local Similarity 85.1%; Pred. No. 0.064;
Matches 40; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| || |  || |||||||| |||||||||||||||||||| |
Db        699 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAATA 653
```

Search completed: March 2, 2004, 11:51:36
Job time : 22.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:30:03 ; Search time 2156 Seconds
(without alignments)
706.387 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	1353	29	AY416856	AY416856 Homo sapi
2	42	82.4	872	29	ECAA2BAR	AL606560 Horse alp
c 3	41.6	81.6	430	28	AZ223727	AZ223727 RPCI-23-6
c 4	41.6	81.6	469	9	AA943361	AA943361 EST198860
c 5	41.6	81.6	517	10	BE097734	BE097734 UI-R-BO1-
c 6	41.6	81.6	552	14	CF795982	CF795982 892192 MA
c 7	41.6	81.6	604	9	AJ517718	AJ517718 AJ517718
c 8	41.6	81.6	713	28	AZ288043	AZ288043 RPCI-23-1
9	40.6	79.6	640	12	BI067787	BI067787 pgf1n.pk0
c 10	40.6	79.6	668	28	BH309086	BH309086 CH230-4L1
11	40.6	79.6	723	13	BU121352	BU121352 603146064
12	40.6	79.6	753	10	BE613618	BE613618 601504406
13	40.6	79.6	797	28	AQ875889	AQ875889 V130F6 mT
c 14	40.6	79.6	826	28	BZ227940	BZ227940 CH230-400
15	40.6	79.6	873	13	BQ231724	BQ231724 AGENCOURT
16	40.6	79.6	1362	12	BM807097	BM807097 AGENCOURT
17	40.4	79.2	453	10	BB852469	BB852469 BB852469
18	40.4	79.2	553	13	BX519271	BX519271 BX519271
19	40.4	79.2	786	28	AZ208950	AZ208950 SP_0138_A
20	40.4	79.2	799	28	BZ152227	BZ152227 CH230-504
21	40.4	79.2	834	28	BZ249816	BZ249816 CH230-447
22	40	78.4	152	28	BH108383	BH108383 RPCI-24-4
23	40	78.4	167	28	BH072396	BH072396 RPCI-24-2
c 24	40	78.4	256	14	CA315228	CA315228 UI-M-FW0-
c 25	40	78.4	330	14	CF897938	CF897938 A0231H07-
c 26	40	78.4	331	9	AL135731	AL135731 DKFZp434H
c 27	40	78.4	358	14	CD564037	CD564037 B0473A03-
c 28	40	78.4	365	13	BY054209	BY054209 BY054209
c 29	40	78.4	365	13	BY168255	BY168255 BY168255
c 30	40	78.4	373	14	CA538239	CA538239 C0264C01-
c 31	40	78.4	388	13	BY135560	BY135560 BY135560
c 32	40	78.4	413	28	BZ105773	BZ105773 CH230-153
c 33	40	78.4	444	13	BQ558077	BQ558077 H4050A07-
34	40	78.4	446	10	BG076252	BG076252 H3157D11-
35	40	78.4	459	28	AZ554793	AZ554793 RPCI-23-2
c 36	40	78.4	476	10	BB851808	BB851808 BB851808
c 37	40	78.4	512	14	CB272922	CB272922 mai64d07.
c 38	40	78.4	514	28	BZ089457	BZ089457 CH230-1C1
c 39	40	78.4	517	14	CB716103	CB716103 AMGNNUC:N
c 40	40	78.4	558	28	BZ159900	BZ159900 CH230-376
c 41	40	78.4	578	14	CA752540	CA752540 UI-M-FO0-
c 42	40	78.4	586	9	AI451753	AI451753 mb16f09.y
43	40	78.4	587	12	BG325179	BG325179 602423735
c 44	40	78.4	594	14	CF796838	CF796838 NcESTqab8
45	40	78.4	612	28	BZ149404	BZ149404 CH230-395

ALIGNMENTS

RESULT 1
AY416856
LOCUS AY416856 1353 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM6030 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY416856
VERSION AY416856.1 GI:39772816
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1353)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1353)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

```
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
  COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
  FEATURES             Location/Qualifiers
       source          1. .1353
                       /organism="Homo sapiens"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9606"
       gene            <1. .>1353
                       /locus_tag="HCM6030"
  ORIGIN

    Query Match             100.0%;  Score 51;  DB 29;  Length 1353;
    Best Local Similarity   100.0%;  Pred. No. 0.7;
    Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGT 930


  RESULT 2
  ECAA2BAR
  LOCUS       ECAA2BAR                  872 bp    DNA     linear   GSS 14-SEP-2001
  DEFINITION  Horse alpha2 adrenergic receptor gene fragment probably subtype b,
              genomic survey sequence.
  ACCESSION   AL606560
  VERSION     AL606560.1  GI:15591917
  KEYWORDS    GSS; Alpha2 adrenergic receptor gene.
  SOURCE      Equus caballus (horse)
    ORGANISM  Equus caballus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
  REFERENCE   1  (bases 1 to 872)
    AUTHORS   Hunter,C. and Elgar,G.
    TITLE     Alpha2 adrenergic receptor gene
    JOURNAL   Unpublished
  REFERENCE   2  (bases 1 to 872)
    AUTHORS   Hunter,C.
    TITLE     Direct Submission
    JOURNAL   Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
              Centre Hinxton, Cambridge, CB10 1SB. UK Email:
              biohelp@hgmp.mrc.ac.uk
  FEATURES             Location/Qualifiers
       source          1. .872
                       /organism="Equus caballus"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:9796"
  ORIGIN

    Query Match             82.4%;  Score 42;  DB 29;  Length 872;
    Best Local Similarity   90.0%;  Pred. No. 39;
    Matches   45;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTG 50
              ||||| |||||||||||||||| || |||||||||||||||||| ||| |
Db        571 GAGGAGGAAGCTGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGG 620


  RESULT 3
  AZ223727/c
  LOCUS       AZ223727                  430 bp    DNA     linear   GSS 14-JUN-2000
  DEFINITION  RPCI-23-63A7.TJ RPCI-23 Mus musculus genomic clone RPCI-23-63A7,
              genomic survey sequence.
  ACCESSION   AZ223727
  VERSION     AZ223727.1  GI:8531776
  KEYWORDS    GSS.
  SOURCE      Mus musculus (house mouse)
    ORGANISM  Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE   1  (bases 1 to 430)
    AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
              Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
              Jong,P. and Fraser,C.M.
    TITLE     Mouse BAC End Sequences from Library RPCI-23
    JOURNAL   Unpublished (1999)
  COMMENT     Other_GSSs: RPCI-23-63A7.TV
              Contact: Shaying Zhao
              Department of Eukaryotic Genomics
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 0200
              Fax: 301 838 0208
              Email: szhao@tigr.org
              Clones are derived from the mouse BAC library RPCI-23. For BAC
              library availability, please contact Pieter de Jong
              (pieter@dejong.med.buffalo.edu). Clones may be purchased from
              BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
              or from Resea ch Genetics (info@resgen.com). BAC end page:
              http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
              Plate: 63  row: A  column: 7
              Seq primer: SP6
              Class: BAC ends.
  FEATURES             Location/Qualifiers
       source          1. .430
                       /organism="Mus musculus"
                       /mol_type="genomic DNA"
                       /strain="C57BL/6J"
                       /db_xref="taxon:10090"
                       /clone="RPCI-23-63A7"
                       /sex="Female"
                       /lab_host="DH10B"
                       /clone_lib="RPCI-23"
                       /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                       EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                       brain genomic DNA was isolated and  partially digested
                       with a combination of EcoRI and EcoRI Methylase.   Size
                       selected DNA was cloned into the pBACe3.6 vector at the
                       EcoRI  sites.  The ligation products were transformed into
                       DH10B  electrocompetent cells (BRL Life Technologies).  "
  ORIGIN

    Query Match             81.6%;  Score 41.6;  DB 28;  Length 430;
    Best Local Similarity   91.7%;  Pred. No. 43;
    Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  || ||||||||||||||||||||||||||||||||||
Db        103 GAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 56


  RESULT 4
  AA943361/c
  LOCUS       AA943361                  469 bp    mRNA    linear   EST 16-JUN-1998
  DEFINITION  EST198860 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
              RBRAI64 3' end, mRNA sequence.
  ACCESSION   AA943361
  VERSION     AA943361.1  GI:3103277
  KEYWORDS    EST.
  SOURCE      Rattus sp.
    ORGANISM  Rattus sp.
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
  REFERENCE   1  (bases 1 to 469)
    AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
              Kerlavage,A.R. and Adams,M.D.
    TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
              Gene Index
    JOURNAL   Unpublished (1998)
  COMMENT     Contact: Lee, NH
              The Institute for Genomic Research
              9712, Medical Center Drive, Rockville, MD 20850, USA
              Tel: (301)-838-3529
```

```
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES              Location/Qualifiers
     source           1. .469
                      /organism="Rattus sp."
                      /mol_type="mRNA"
                      /db_xref="ATCC (inhost):2012877"
                      /db_xref="taxon:10118"
                      /clone="RBRAI64"
                      /clone_lib="Normalized rat brain, Bento Soares"
                      /note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
                      Site_2: NotI"
ORIGIN

  Query Match             81.6%;  Score 41.6;  DB 9;  Length 469;
  Best Local Similarity   91.7%;  Pred. No. 43;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || || ||||| |||||||||||||||||||||||||||||||||| |||
Db        403 GAAGAAGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAG 356


RESULT 5
BE097734/c
LOCUS       BE097734                517 bp    mRNA    linear   EST 12-JUN-2000
DEFINITION  UI-R-BO1-aqb-a-11-0-UI.s1 UI-R-BO1 Rattus norvegicus cDNA clone
            UI-R-BO1-aqb-a-11-0-UI 3', mRNA sequence.
ACCESSION   BE097734
VERSION     BE097734.1  GI:8488660
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized corpus-striatum library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com) The following repetitive
            elements were found in this cDNA sequence: 365-436,
            >(GGA)n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .517
                      /organism="Rattus norvegicus"
                      /mol_type="mRNA"
                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
                      /clone="UI-R-BO1-aqb-a-11-0-UI"
                      /dev_stage="adult"
                      /lab_host="DH10B (Life Technologies)"
                      /clone_lib="UI-R-BO1"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The library
                      (UI-R-BO1) is a subtracted library derived from a mixture
                      of the following tissues: thalamus, cerebellum,
                      hypothalamus, medulla, pons, midbrain, cerebral cortex,
                      corpus striatum and hippocampus. For a detailed
                      description of the library from which this clone was
                      derived, please visit our web site at
                      ratest.eng.uiowa.edu. The subtraction has been previously
                      described in (Bonaldo, Lennon and Soares, Genome Research
                      6:791-806, 1996)
                      TAG_TISSUE=corpus-striatum
                      TAG_LIB=UI-R-BO1
                      TAG_SEQ=CTAGG"
ORIGIN

  Query Match             81.6%;  Score 41.6;  DB 10;  Length 517;
  Best Local Similarity   91.7%;  Pred. No. 44;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              || || ||||| |||||||||||||||||||||||||||||||||| |||
Db        420 GAAGAAGAAGCAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAG 373


RESULT 6
CF795982/c
LOCUS       CF795982                552 bp    mRNA    linear   EST 21-OCT-2003
DEFINITION  892192 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION   CF795982
VERSION     CF795982.1  GI:37800555
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
  TITLE     Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: TMW8018  row: D  column: 17
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES              Location/Qualifiers
     source           1. .552
                      /organism="Sus scrofa"
                      /mol_type="mRNA"
                      /db_xref="taxon:9823"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /clone_lib="MARC 4PIG"
                      /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                      Library made with combined RNA from day-10, day-13,
                      day-15, day-25, and day-30 whole embryos."
ORIGIN

  Query Match             81.6%;  Score 41.6;  DB 14;  Length 552;
  Best Local Similarity   91.7%;  Pred. No. 44;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              |||||||||| |||||||||||| |||||||| |||||||| ||||||
Db        152 GAGGATGAAGATGAAGAGGAGGACGAGGAGGACGAGGAGGATGAAGAG 105
```

```
RESULT 7
AJ517718/c
LOCUS       AJ517718                604 bp    mRNA    linear   EST 27-NOV-2002
DEFINITION  AJ517718 Dreissena polymorpha mRNA Dreissena polymorpha cDNA clone
            chron35, mRNA sequence.
ACCESSION   AJ517718
VERSION     AJ517718.1  GI:25778429
KEYWORDS    EST.
SOURCE      Dreissena polymorpha
  ORGANISM  Dreissena polymorpha
            Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
            Dreissenoidea; Dreissenidae; Dreissena.
REFERENCE   1  (bases 1 to 604)
  AUTHORS   Bultelle,F., Panchout,M., Leboulenger,F. and Danger,J.-M.
  TITLE     Effect of xenobiotics on the transcriptome of the zebra mussel
            Dreissena polymorpha
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Danger J-M
            Laboratory of Ecotoxicology
            University of Le Havre
            25 rue P. Lebon, 76058 Le Havre CEDEX, France.
FEATURES             Location/Qualifiers
     source          1. .604
                     /organism="Dreissena polymorpha"
                     /mol_type="mRNA"
                     /db_xref="taxon:45954"
                     /clone="chron35"
                     /clone_lib="Dreissena polymorpha mRNA"
ORIGIN

  Query Match           81.6%;  Score 41.6;  DB 9;  Length 604;
  Best Local Similarity  91.7%;  Pred. No. 45;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  |||||||||||||| ||||||||||||||||||||
Db         87 GAGGACGAAGAGGAAGAGGAGGAAGATGAGGAGGAGGAGGAGGAAGAG 40


RESULT 8
AZ288043/c
LOCUS       AZ288043                713 bp    DNA     linear   GSS 27-JUL-2000
DEFINITION  RPCI-23-102K10.TV RPCI-23 Mus musculus genomic clone
            RPCI-23-102K10, genomic survey sequence.
ACCESSION   AZ288043
VERSION     AZ288043.1  GI:9529829
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
            Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
            Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-102K10.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 102  row: K  column: 10
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-102K10"
                     /sex="Female"
                     /lab_host="DH10B"
                     /clone_lib="RPCI-23"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies).  "
ORIGIN

  Query Match           81.6%;  Score 41.6;  DB 28;  Length 713;
  Best Local Similarity  91.7%;  Pred. No. 46;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 48
              ||||| ||||  || ||||||||||||||||||||||||||||||||||
Db        101 GAGGAGGAAGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 54


RESULT 9
BI067787
LOCUS       BI067787                640 bp    mRNA    linear   EST 15-JUN-2001
DEFINITION  pgf1n.pk007.l24 normalized chicken fat cDNA library Gallus gallus
            cDNA clone pgf1n.pk007.l24 5' similar to gi|4506411
            ref|NP_002874.1| Ran GTPase activating protein 1; Fug1 [Homo
            sapiens] gi|11418178 ref|XP_010014.1| Ran GTPase activating protein
            1 [Homo sapiens] sp|P46060|RGP1_HUMAN RAN-GTPASE ACTIVATING PROTEIN
            1 pir|I38146 RanGAP1 - human pir|JC, mRNA sequence.
ACCESSION   BI067787
VERSION     BI067787.1  GI:14475309
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 640)
  AUTHORS   Cogburn,L.A., Morgan,R.W. and Burnside,J.
  TITLE     Chicken ESTs from fat
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Larry A. Cogburn
            University of Delaware
            Townsend Hall, Newark, DE 19717, USA
            Tel: 302-831-1335
            Fax: 302-831-2822
            Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES             Location/Qualifiers
     source          1. .640
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9031"
                     /clone="pgf1n.pk007.l24"
                     /sex="Male and Female"
                     /tissue_type="fat"
                     /lab_host="E.coli EMDH10B"
                     /clone_lib="normalized chicken fat cDNA library"
                     /note="Vector: pSPORT1"
ORIGIN

  Query Match           79.6%;  Score 40.6;  DB 12;  Length 640;
  Best Local Similarity  91.5%;  Pred. No. 71;
```

```
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              || || |||| |||||| ||||||||||||||||||||||||||||||
Db        180 GAAGAGGAAGATGAAGAAGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 226


RESULT 10
BH309086/c
LOCUS       BH309086                668 bp    DNA     linear   GSS 03-DEC-2001
DEFINITION  CH230-4L16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
            CH230-4L16, genomic survey sequence.
ACCESSION   BH309086
VERSION     BH309086.1  GI:17234555
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 668)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 EcoRI segment
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 4  row: L  column: 16
            Seq primer: T7
            Class: BAC ends.
FEATURES              Location/Qualifiers
     source           1. .668
                      /organism="Rattus norvegicus"
                      /mol_type="genomic DNA"
                      /strain="BN/SsNHsd/MCW"
                      /db_xref="taxon:10116"
                      /clone="CH230-4L16"
                      /sex="Female"
                      /cell_type="Brain"
                      /clone_lib="CHORI-230 Segment 1"
                      /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                      CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                      Pieter de Jong"
ORIGIN

  Query Match             79.6%;  Score 40.6;  DB 28;  Length 668;
  Best Local Similarity   91.5%;  Pred. No. 71;
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| ||||  ||||||||||||||||||||||||||||| |||||
Db        164 GAGGAGGAAGAAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAAGA 118


RESULT 11
BU121352
LOCUS       BU121352                723 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  603146064F1 CSEQCHL17 Gallus gallus cDNA clone ChEST145o16 5', mRNA
            sequence.
ACCESSION   BU121352
VERSION     BU121352.1  GI:25331126
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES              Location/Qualifiers
     source           1. .723
                      /organism="Gallus gallus"
                      /mol_type="mRNA"
                      /strain="Compton Line 15I"
                      /db_xref="taxon:9031"
                      /clone="ChEST145o16"
                      /sex="Female"
                      /dev_stage="adult"
                      /lab_host="DH10B"
                      /clone_lib="CSEQCHL17"
                      /note="Organ: kidney + adrenal; Vector: pBluescript II
                      KS(+); Site_1: EcoRI; Site_2: Not1; Modification of
                      pBluescript II KS(+) [Stratagene] vector to accommodate
                      cDNA produced with the T-trimmed protocol (Construction of
                      uni-directionally cloned cDNA libraries from messenger RNA
                      for improved 3' end DNA sequencing by Glenn Fu, et al.
                      U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
                      NotI and EcoRI. Ligate in double stranded adaptor
                      containing BsgI and BamHI sites
                      [5'ggccgcgtgcagccccggatccgaaaaaaag]
                      [5'aattcttttttcggatccggggctgcacgc]"
ORIGIN

  Query Match             79.6%;  Score 40.6;  DB 13;  Length 723;
  Best Local Similarity   91.5%;  Pred. No. 72;
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              || || |||| |||||| ||||||||||||||||||||||||||||||
Db        648 GAAGAGGAAGATGAAGAAGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 694


RESULT 12
BE613618
LOCUS       BE613618                753 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601504406F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906193 5',
            mRNA sequence.
ACCESSION   BE613618
VERSION     BE613618.1  GI:9895215
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
```

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9714 row: 1 column: 02
High quality sequence stop: 711.

FEATURES Location/Qualifiers
source 1. .753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3906193"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "

ORIGIN

Query Match 79.6%; Score 40.6; DB 10; Length 753;
Best Local Similarity 91.5%; Pred. No. 72;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
||||| |||| || ||||||||||||||||||||||||||||||||||||
Db 27 GAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 73

RESULT 13
AQ875889
LOCUS AQ875889 797 bp DNA linear GSS 08-NOV-1999
DEFINITION V130F6 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence.
ACCESSION AQ875889
VERSION AQ875889.1 GI:6288133
KEYWORDS GSS.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 797)
AUTHORS Ross-Macdonald,P., Roemer,T., Coelho,P.S.R., Agarwal,S., Kumar,A., desEtages,S.A., Cheung,K.-H., Sheehan,A., Symoniatis,D., Jansen,R., Umansky,L., Heidtman,M., Nelson,K., Iwasaki,H., Kanada,D., Lugo,R., Hager,K., Miller,P., Roeder,G.S. and Snyder,M.
TITLE Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption
JOURNAL Unpublished (1999)
COMMENT Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seq primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.

FEATURES Location/Qualifiers
source 1. .797
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
/lab_host="E. coli"
/clone_lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library without 2 micron or mitochondrial DNA was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was subsequently mutagenized with a mTn-3xHA/lacZ minitransposon containing lacZ, URA3, and tet resistance. "

ORIGIN

Query Match 79.6%; Score 40.6; DB 28; Length 797;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
|| ||||||| |||||||||||| |||||||||||||||||||||||
Db 260 GAAGATGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGA 306

RESULT 14
BZ227940/c
LOCUS BZ227940 826 bp DNA linear GSS 12-OCT-2002
DEFINITION CH230-400D22.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-400D22, genomic survey sequence.
ACCESSION BZ227940
VERSION BZ227940.1 GI:23886481
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 826)
AUTHORS Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment
JOURNAL Unpublished (1999)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 400 row: D column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES Location/Qualifiers
source 1. .826
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-400D22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI; CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by Pieter de Jong"

ORIGIN

Query Match 79.6%; Score 40.6; DB 28; Length 826;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
||||| || | ||||||||||||||||||||||||||||||||||||||
Db 794 GAGGAAGAGGAAGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 748

RESULT 15
BQ231724
LOCUS BQ231724 873 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7560029 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055864 5', mRNA sequence.
ACCESSION BQ231724
VERSION BQ231724.1 GI:20413124
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 873)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13316 row: m column: 17
High quality sequence stop: 703.
FEATURES Location/Qualifiers
source 1. .873
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6055864"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."
ORIGIN

Query Match 79.6%; Score 40.6; DB 13; Length 873;
Best Local Similarity 91.5%; Pred. No. 74;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 47
              ||||| ||||  || ||||||||||||||||||||||||||||||||
Db        103 GAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGA 149
```

Search completed: March 2, 2004, 08:34:35
Job time : 2156 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 04:47:22 ; Search time 864.5 Seconds
(without alignments)
2556.963 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		51	100.0	246	10	S67317S2	S67319 alpha 2-adr
2		51	100.0	828	10	S67316	S67316 alpha 2-adr
3		51	100.0	1344	6	AX350490	AX350490 Sequence
4		51	100.0	1344	9	AF316895	AF316895 Homo sapi
5	c	51	100.0	22842	9	AC092603	AC092603 Homo sapi
6		46.2	90.6	1168	4	PVI251176	AJ251176 Phoca vit
7		43	84.3	1180	4	LPA505821	AJ505821 Lama paco
8		43	84.3	1197	4	LPA315941	AJ315941 Lama paco
9		41.8	82.0	6904	6	AX344976	AX344976 Sequence
10		41.8	82.0	6904	6	AX348497	AX348497 Sequence
11		41.6	81.6	885	9	HUMA2C2	M38742 Human alpha
12	c	41.6	81.6	1030	9	HSA325747	AJ325747 Homo sapi
13		41.6	81.6	1353	6	AX350489	AX350489 Sequence
14		41.6	81.6	2072	6	AR270618	AR270618 Sequence
15		41.6	81.6	2072	9	HUMADRA2RA	M34041 Human alpha
16		41.6	81.6	3274	6	AX548756	AX548756 Sequence
17		41.6	81.6	9944	9	AF005900	AF005900 Homo sapi
18		41.4	81.2	1180	9	NCO251186	AJ251186 Nycticebu
19		41.4	81.2	1218	10	TTA427262	AJ427262 Thomomys
20		39.8	78.0	1179	10	TFA427266	AJ427266 Trichys f
21		38.8	76.1	1347	10	AF332049	AF332049 Mus muscu
22		38.8	76.1	1347	10	AF332050	AF332050 Mus muscu
23		38.8	76.1	1650	10	MUSAADRENH	L00979 Mus musculu
24		38.8	76.1	2319	10	RATA2BR	M32061 Rat alpha-2
25		38.8	76.1	6268	10	AF366899	AF366899 Rattus no
26		38.8	76.1	9377	10	MUSADRRECA	M94583 Mus musculu
27		38.8	76.1	83802	10	AL731836	AL731836 Mouse DNA
28		38.8	76.1	124474	2	AC126878	AC126878 Rattus no
29		38.8	76.1	261258	2	AC091365	AC091365 Rattus no
30		38.8	76.1	276543	2	AC112830	AC112830 Rattus no
31		38.4	75.3	1639	10	RNA2BARA	X74400 R.norvegicu
32		38.2	74.9	1173	4	EAT419810	AJ419810 Emballonu
33		38.2	74.9	1180	10	CPO271336	AJ271336 Cavia por
34		38.2	74.9	1188	4	RTU419814	AJ419814 Rhogeessa
35		38.2	74.9	1198	4	ECAAR2B	Y15945 Equus cabal.
36		38.2	74.9	1356	4	AY150333	AY150333 Tupaia be
37	c	37.2	72.9	194614	2	AC113944	AC113944 Mus muscu
38	c	37	72.5	301817	2	AC095571	AC095571 Rattus no
39		36.6	71.8	1180	4	HAM251178	AJ251178 Hippopota
40		36.6	71.8	1185	10	EDO427270	AJ427270 Erethizon
41		36.6	71.8	1185	10	ASP427259	AJ427259 Anomaluru
42		36.6	71.8	1203	4	TTE315939	AJ315939 Tapirus t
43		36.4	71.4	1547	10	AY341886	AY341886 Rattus no
44		36.4	71.4	143350	2	AC121509	AC121509 Mus muscu
45		36.4	71.4	241678	2	AC121484	AC121484 Rattus no

ALIGNMENTS

RESULT 1
S67317S2
LOCUS S67317S2 246 bp mRNA linear ROD 26-FEB-1994
DEFINITION alpha 2-adrenergic receptor [rats, Sprague-Dawley, 5 month old pancreas, mRNA Partial, 246 nt, segment 2 of 2].
ACCESSION S67319
VERSION S67319.1 GI:456951
KEYWORDS .
SEGMENT 2 of 2
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 246)

```
  AUTHORS   Wang,S.Y. and Pilkey,D.T.
  TITLE     Identification in islets of Langerhans of a new rat alpha
            2-adrenergic receptor
  JOURNAL   Diabetes 43 (1), 127-136 (1994)
  MEDLINE   94085695
   PUBMED   8262309
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 140733] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES             Location/Qualifiers
     source          1. .246
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
     gene            order(S67317.1:1. .130,1. .246)
                     /gene="alpha 2-adrenergic receptor"
ORIGIN

  Query Match           100.0%;  Score 51;  DB 10;  Length 246;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         13 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 63


RESULT 2
S67316
LOCUS       S67316                   828 bp    mRNA    linear   ROD 21-APR-2003
DEFINITION  alpha 2-adrenergic receptor [rats, Sprague-Dawley, islets of
            Langerhans, mRNA Partial, 828 nt].
ACCESSION   S67316
VERSION     S67316.1  GI:456949
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Wang,S.Y. and Pilkey,D.T.
  TITLE     Identification in islets of Langerhans of a new rat alpha
            2-adrenergic receptor
  JOURNAL   Diabetes 43 (1), 127-136 (1994)
  MEDLINE   94085695
   PUBMED   8262309
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 140730] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Rattus sp."
                     /mol_type="mRNA"
                     /db_xref="taxon:10118"
     CDS             <1. .>828
                     /note="This sequence comes from Fig. 1"
                     /codon_start=1
                     /product="alpha 2-adrenergic receptor"
                     /protein_id="AAP14006.1"
                     /db_xref="GI:30027780"
                     /translation="CTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLI
                     AAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYL
                     IAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKSTGE
                     KEEGETPEDTGTRALPASWAALPNSGQGQKEGVCGGSPEDEAEEEEEEEECEPQAVP
                     VSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLA
                     "
ORIGIN

  Query Match           100.0%;  Score 51;  DB 10;  Length 828;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 645


RESULT 3
AX350490
LOCUS       AX350490                 1344 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 2 from Patent WO0179561.
ACCESSION   AX350490
VERSION     AX350490.1  GI:18616092
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liggett,S.B. and Small,K.M.
  TITLE     Alpha-2 adrenergic receptor polymorphisms
  JOURNAL   Patent: WO 0179561-A 2 25-OCT-2001;
            Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES             Location/Qualifiers
     source          1. .1344
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 51;  DB 6;  Length 1344;
  Best Local Similarity  100.0%;  Pred. No. 7e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930


RESULT 4
AF316895
LOCUS       AF316895                 1344 bp    DNA     linear   PRI 13-FEB-2001
DEFINITION  Homo sapiens alpha 2B adrenergic receptor (ADRA2B) gene, complete
            cds.
ACCESSION   AF316895
VERSION     AF316895.1  GI:12698669
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1344)
  AUTHORS   Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B.
  TITLE     Polymorphic deletion of three intracellular acidic residues of the
            alpha 2B-adrenergic receptor decreases G protein-coupled receptor
            kinase-mediated phosphorylation and desensitization
  JOURNAL   J. Biol. Chem. 276 (7), 4917-4922 (2001)
  MEDLINE   21265012
   PUBMED   11056163
REFERENCE   2  (bases 1 to 1344)
  AUTHORS   Small,K.M., Brown,K.M., Forbes,S.L. and Liggett,S.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-OCT-2000) Internal Medicine, University of
            Cincinnati, 231 Bethesda Ave, Cincinnati, OH 45267, USA
FEATURES             Location/Qualifiers
     source          1. .1344
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
     gene            <1. .>1344
                     /gene="ADRA2B"
     mRNA            <1. .>1344
                     /gene="ADRA2B"
                     /product="alpha 2B adrenergic receptor"
```

```
     CDS             1. .1344
                     /gene="ADRA2B"
                     /note="G-protein coupled receptor"
                     /codon_start=1
                     /product="alpha 2B adrenergic receptor"
                     /protein_id="AAK01635.1"
                     /db_xref="GI:12698670"
                     /translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
                     APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
                     LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRG
                     RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
                     KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
                     LPNSGQGQKEGVCGASPEDEAEEEEEEEECEPQAVPVSPASACSPPLQQPQGSRVLA
                     TLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGA
                     ICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW"
     variation       891^892
                     /gene="ADRA2B"
                     /note="compared to wild type sequence presented in GenBank
                     Accession Number AF005900; polymorphic sequence lacks
                     three glu residues at this location"
                     /frequency="Caucasians 0.31; African-Americans 0.12"
                     /replace="gaagaggag"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 9;  Length 1344;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930


RESULT 5
AC092603/c
LOCUS       AC092603               22842 bp    DNA     linear   PRI 01-MAR-2002
DEFINITION  Homo sapiens BAC clone RP11-139J6 from 2, complete sequence.
ACCESSION   AC092603 AC073396
VERSION     AC092603.2  GI:16303539
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22842)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 22842)
  AUTHORS   Martinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doebber,A.
  TITLE     The sequence of Homo sapiens BAC clone RP11-139J6
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 22842)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 22842)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 22842)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 22842)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Oct 20, 2001 this sequence version replaced gi:14916188.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0139J06
                Drafting Center: WIBR
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
            the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
            Actual end of this clone is at base position 48999 of RP11-574O17.

            Polymorphisms have been identified between AC013272 and AC092603.

            The sequence of AC073396 has been incorporated into AC092603.
FEATURES                Location/Qualifiers
     source             1. .22842
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="2"
                        /map="2"
                        /clone="RP11-139J6"
                        /clone_lib="RPCI-11"
     repeat_region      352. .465
                        /rpt_family="MIR"
     repeat_region      1377. .1424
                        /rpt_family="(TG)n"
     repeat_region      1424. .1449
                        /rpt_family="(GA)n"
     repeat_region      1495. .1665
                        /rpt_family="Alu"
     repeat_region      1669. .1966
                        /rpt_family="Alu"
     repeat_region      2812. .2918
                        /rpt_family="MIR"
```

```
repeat_region   3183. .3448
                /rpt_family="CT-rich"
repeat_region   5541. .5566
                /rpt_family="AT_rich"
repeat_region   5576. .5870
                /rpt_family="Alu"
repeat_region   5873. .6183
                /rpt_family="Alu"
repeat_region   6195. .6301
                /rpt_family="MIR"
repeat_region   6627. .6733
                /rpt_family="L2"
repeat_region   7278. .7415
                /rpt_family="MIR"
repeat_region   7698. .7723
                /rpt_family="(GGCTG)n"
repeat_region   8140. .8218
                /rpt_family="G-rich"
repeat_region   8863. .8922
                /rpt_family="MIR"
repeat_region   9191. .9346
                /rpt_family="MIR"
repeat_region   10172. .10296
                /rpt_family="MIR"
repeat_region   10436. .10550
                /rpt_family="MIR"
repeat_region   11016. .11169
                /rpt_family="MIR"
repeat_region   11617. .11882
                /rpt_family="L2"
misc_feature    12062. .12532
                /note="match to EST AI733093 (NID:g5054206) oj40h05.x5"
misc_feature    12062. .12257
                /note="match to EST AA887330 (NID:g3002438) oj40h05.s1"
misc_feature    12378. .12902
                /note="match to EST AI791589 (NID:g5339305) oj40h05.y5"
misc_feature    13059
                /note="match to EST BF475329 (NID:g11546156)"
misc_feature    13072. .13459
                /note="match to EST BF475329 (NID:g11546156)"
misc_feature    14030. .14244
                /note="similar to Homo sapiens EST T39448 (NID:g647179)
                ya06a09.r2"
misc_feature    14060. .14247
                /note="similar to Homo sapiens EST AL549866
                (NID:g12886265)"
misc_feature    14060. .14247
                /note="similar to Homo sapiens EST AL573897
                (NID:g12933576)"
repeat_region   14413. .14439
                /rpt_family="(TCC)n"
misc_feature    14762. .14822
                /note="similar to Homo sapiens EST AL544609
                (NID:g12877089)"
misc_feature    14849. .16413
                /note="CpG_island (%GC=74.2, o/e=0.90, #CpGs=191)"
misc_feature    14900. .15218
                /note="similar to Homo sapiens EST AL544609
                (NID:g12877089)"
misc_feature    15084. .15487
                /note="similar to Sus scrofa EST AW785035 (NID:g7841811)"
misc_feature    15110. .15648
                /note="similar to Rattus norvegicus EST AW916723
                (NID:g8082456)"
repeat_region   15747. .15832
                /rpt_family="G-rich"
repeat_region   18481. .18596
                /rpt_family="L2"
repeat_region   19266. .19675
                /rpt_family="L2"
repeat_region   20027. .20223
                /rpt_family="MER1_type"
repeat_region   20316. .20416
                /rpt_family="L2"
repeat_region   20537. .20973
                /rpt_family="L2"
misc_feature    22057. .22471
                /note="match to EST AA830781 (NID:g2903880) oc56b01.s1"
misc_feature    22057. .22208
                /note="match to EST AA836522 (NID:g2910841) od22d08.s1"
ORIGIN
```

Query Match 100.0%; Score 51; DB 9; Length 22842;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14451 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 14401
```

```
RESULT 6
PVI251176
LOCUS       PVI251176                1168 bp    DNA     linear   MAM 01-JUN-2001
DEFINITION  Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B.
ACCESSION   AJ251176
VERSION     AJ251176.1  GI:11322419
KEYWORDS    aar2B gene; alpha adrenergic receptor 2B.
SOURCE      Phoca vitulina (harbor seal)
  ORGANISM  Phoca vitulina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
REFERENCE   1
  AUTHORS   Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adkins,R.,
            Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
  TITLE     Parallel adaptive radiations in two major clades of placental
            mammals
  JOURNAL   Nature 409 (6820), 610-614 (2001)
  MEDLINE   21082081
   PUBMED   11214318
REFERENCE   2  (bases 1 to 1168)
  AUTHORS   Madsen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-1999) Madsen O., Department of Biochemistry,
            University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
            NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1168
                     /organism="Phoca vitulina"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9720"
     gene            1. .1168
                     /gene="aar2B"
     CDS             <1. .>1168
                     /gene="aar2B"
                     /codon_start=2
                     /product="alpha adrenergic receptor 2B"
                     /protein_id="CAC16696.1"
                     /db_xref="GI:11322420"
                     /db_xref="GOA:Q9GL07"
                     /db_xref="SPTREMBL:Q9GL07"
                     /translation="AIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
                     RALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPAGAPQCKLNQEAWYI
                     LASSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPGAKGGPGPGESKQPRSVPTGTSTK
                     LPTLASLAASEEANGHSKPTGEKEGDTPEDPGTPALPPSWSALPSSGQSQKEGVCGAS
                     PEEEAEEEEEEEECEPQALPASPASACSPPLPQPQGSRVLATLRGQVLLGRGVGTAS
                     GQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQHCKVPHGLF"
ORIGIN
```

Query Match 90.6%; Score 46.2; DB 4; Length 1168;
Best Local Similarity 94.1%; Pred. No. 0.0017;
Matches 48; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| |||||||||||||||||||||||||||||||||| || |||
```

```
Db        833 GAGGAGGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAGCCTCAG 883


RESULT 7
LPA505821
LOCUS       LPA505821               1180 bp    DNA     linear   MAM 12-DEC-2002
DEFINITION  Lama pacos partial adra2b gene for alpha 2B adrenergic receptor,
            adra2b-2 allele.
ACCESSION   AJ505821
VERSION     AJ505821.1  GI:22324219
KEYWORDS    adra2b gene; alpha 2B adrenergic receptor.
SOURCE      Lama pacos (alpaca)
  ORGANISM  Lama pacos
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
REFERENCE   1
  AUTHORS   Madsen,O., Willemsen,D., Ursing,B.M., Arnason,U. and de Jong,W.W.
  TITLE     Molecular evolution of the mammalian alpha 2B adrenergic receptor
  JOURNAL   Mol. Biol. Evol. 19 (12), 2150-2160 (2002)
  MEDLINE   22337198
   PUBMED   12446807
REFERENCE   2
  AUTHORS   Madsen,O., Willemsen,D., Ursing,B.M., Arnason,U. and de Jong,W.W.
  TITLE     Molecular evolution of the alpha 2B adrenergic receptor
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1180)
  AUTHORS   Madsen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-AUG-2002) Madsen O., 161 Biochemistry NWI, University
            of Nijmegen, PO.BOX 9101, 6500HB Nijmegen, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1180
                     /organism="Lama pacos"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:30538"
     gene            2. .1180
                     /gene="adra2b"
     CDS             <2. .>1180
                     /gene="adra2b"
                     /codon_start=1
                     /allele="adra2b-2"
                     /product="alpha 2B adrenergic receptor"
                     /protein_id="CAD44322.1"
                     /db_xref="GI:22324220"
                     /db_xref="GOA:Q8MIE1"
                     /db_xref="SPTREMBL:Q8MIE1"
                     /translation="AIAAVITFLILFTIFXNALVILAVLTSRSLRAPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
                     RALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQSPQPRGRPQCKLNQEAWYI
                     LASSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPRAKGGPGKGDSKQPCRIPGEVSAS
                     GKLPTLVSQLATAGEANGRPHPTGEKDEGETPEDPGTPALPPNWPALPNSGQGQKEGV
                     CGTSPEEEAAEEEEEEEECEPQALPASPASACSPPLQQPQVSRVLATLRGQVLLGRGV
                     GTSRGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPEHCKVPRGL
                     F"
ORIGIN

  Query Match             84.3%;  Score 43;  DB 4;  Length 1180;
  Best Local Similarity   90.2%;  Pred. No. 0.014;
  Matches   46;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| || |||| |||||||||||||||||||||||||||| || |||
Db        845 GAGGAGGAGGCTGCAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAGCCTCAG 895


RESULT 8
LPA315941
LOCUS       LPA315941               1197 bp    DNA     linear   MAM 22-MAY-2002
DEFINITION  Lama pacos partial adra2b gene for alpha 2B adrenergic receptor.
ACCESSION   AJ315941
VERSION     AJ315941.1  GI:21212927
KEYWORDS    adra2b gene; alpha 2B adrenergic receptor.
SOURCE      Lama pacos (alpaca)
  ORGANISM  Lama pacos
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
REFERENCE   1
  AUTHORS   Murphy,W.J., Eizirik,E., O'Brien,S.J., Madsen,O., Scally,M.,
            Douady,C.J., Teeling,E., Ryder,O.A., Stanhope,M.J., de Jong,W.W.
            and Springer,M.S.
  TITLE     Resolution of the early placental mammal radiation using Bayesian
            phylogenetics
  JOURNAL   Science 294 (5550), 2348-2351 (2001)
  MEDLINE   21608557
   PUBMED   11743200
REFERENCE   2  (bases 1 to 1197)
  AUTHORS   Madsen,O.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-AUG-2001) Madsen O., 161 Biochemistry NWI, University
            of Nijmegen, P.O.Box 9101, 6500 HB Nijmegen, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1197
                     /organism="Lama pacos"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:30538"
     gene            1. .1197
                     /gene="adra2b"
     CDS             <1. .>1197
                     /gene="adra2b"
                     /codon_start=1
                     /product="alpha 2B adrenergic receptor"
                     /protein_id="CAC87005.1"
                     /db_xref="GI:21212928"
                     /db_xref="GOA:Q8MK51"
                     /db_xref="SPTREMBL:Q8MK51"
                     /translation="AIAAVITFLILFTIFGNALVILAVLTSRSLRAPQNLFLVSLAAA
                     DILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
                     RALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQSPQPRGRPQCKLNQEAWYI
                     LASSIGSFFAPCLIMILVYLRIYLIAKRSHRRGPRAKGGPGKGDSKQPCRIPGEVSAS
                     GKLPTLVSQLATAGEANGRPHPTGEKDEGETPEDPGTPALPPNWPALPNSGQGQKEGV
                     CGTSPEEEAAEEEEAAEEEEEEEECEPQALPASPASACSPPLQQPQISRVLATLRGQV
                     LLGRGVGTSRGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPEHC
                     KVPRGLF"
ORIGIN

  Query Match             84.3%;  Score 43;  DB 4;  Length 1197;
  Best Local Similarity   90.2%;  Pred. No. 0.014;
  Matches   46;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| || |||| |||||||||||||||||||||||||||| || |||
Db        862 GAGGAGGAGGCTGCAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAGCCTCAG 912


RESULT 9
AX344976
LOCUS       AX344976                6904 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 47 from Patent WO0200928.
ACCESSION   AX344976
VERSION     AX344976.1  GI:18492862
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of diseases associated with the immune system
  JOURNAL   Patent: WO 0200928-A 47 03-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6904
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
```

```
Query Match             82.0%;  Score 41.8;  DB 6;  Length 6904;
Best Local Similarity   95.6%;  Pred. No. 0.03;
Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||||||| |||||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 10
AX348497                                6904 bp    DNA     linear   PAT 06-FEB-2002
LOCUS       AX348497
DEFINITION  Sequence 5 from Patent WO0202809.
ACCESSION   AX348497
VERSION     AX348497.1  GI:18614532
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Olek,A., Piepenbrock,C. and Berlin,K.
  TITLE     Diagnosis of behavioural disorders, neurological disorders and
            cancer
  JOURNAL   Patent: WO 0202809-A 5 10-JAN-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .6904
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="chemically treated genomic DNA (Homo sapiens)"

ORIGIN

Query Match             82.0%;  Score 41.8;  DB 6;  Length 6904;
Best Local Similarity   95.6%;  Pred. No. 0.03;
Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||||||| |||||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 11
HUMA2C2                                 885 bp    DNA     linear   PRI 06-MAR-1995
LOCUS       HUMA2C2
DEFINITION  Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cds.
ACCESSION   M38742
VERSION     M38742.1  GI:177867
KEYWORDS    alpha-2 adrenergic receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 885)
  AUTHORS   Chang,A.C., Ho,T.F. and Chang,N.C.
  TITLE     In vitro amplification by polymerase chain reaction of a partial
            gene encoding the third subtype of alpha-2 adrenergic receptor in
            humans
  JOURNAL   Biochem. Biophys. Res. Commun. 172 (2), 817-823 (1990)
  MEDLINE   91054503
   PUBMED   2173582
COMMENT     Original source text: Human adult neuroblastoma DNA, clone PCRA2.
            Draft entry and computer-readable sequence for [Unpublished (1990)]
            kindly submitted
            by A.C.Chang, 20-SEP-1990.
               Institute of Neuroscience
               155, Sect II, Li-Noon St.
               Taipei, Taiwan, 11221 ROC.
FEATURES             Location/Qualifiers
     source          1. .885
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="4p16.3-p15"
                     /clone="PCRA2"
                     /cell_line="neuroblastoma SK-N-SH"
                     /cell_type="neuroblastoma"
                     /tissue_type="neural"
                     /dev_stage="adult"
     gene            1. .885
                     /gene="ADRA2C"
     CDS             1. .885
                     /gene="ADRA2C"
                     /codon_start=1
                     /product="alpha-2-adrenergic receptor"
                     /protein_id="AAA62823.1"
                     /db_xref="GI:177868"
                     /db_xref="GDB:G00-120-540"
                     /translation="PCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWL
                     IAAVISLPPLIYKGDQGPQPRGRPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIY
                     LIAKRSNRRGPRAKGGPGQGESKQPRPDHGGALASAKLPALASVASAREVNGHSKSTG
                     EKEEGETPEDTGTRALPPSWAALPNSGQGQKEGVCGASPEDEAEEEEEEEEEECEP
                     QAVPVSPASACSPPLQQPQGSRVLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFT
                     FVLAVVIGVFVLCWFPFFF"
ORIGIN

Query Match             81.6%;  Score 41.6;  DB 9;  Length 885;
Best Local Similarity   91.7%;  Pred. No. 0.036;
Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || | ||||||||||||||||||||||||||||||||||||
Db        610 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 657


RESULT 12
HSA325747/c                             1030 bp    DNA     linear   PRI 18-JUL-2002
LOCUS       HSA325747
DEFINITION  Homo sapiens genomic sequence surrounding NotI site, clone
            NB1-818S.
ACCESSION   AJ325747
VERSION     AJ325747.1  GI:15870141
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M.,
            Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V.,
            Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I.,
            Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
  TITLE     NotI flanking sequences: a tool for gene discovery and verification
            of the human genome
  JOURNAL   Nucleic Acids Res. 30 (14), 3163-3170 (2002)
  MEDLINE   22131767
   PUBMED   12136098
REFERENCE   2  (bases 1 to 1030)
  AUTHORS   Zabarovsky,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
            Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .1030
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="NB1-818S"

ORIGIN

Query Match             81.6%;  Score 41.6;  DB 9;  Length 1030;
Best Local Similarity   91.7%;  Pred. No. 0.036;
Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||||
Db        187 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 140


RESULT 13
AX350489
LOCUS       AX350489               1353 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 1 from Patent WO0179561.
ACCESSION   AX350489
VERSION     AX350489.1  GI:18616091
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Liggett,S.B. and Small,K.M.
  TITLE     Alpha-2 adrenergic receptor polymorphisms
  JOURNAL   Patent: WO 0179561-A 1 25-OCT-2001;
            Liggett, Stephen B. (US) ; Small, Kersten M. (US)
FEATURES             Location/Qualifiers
     source          1. .1353
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           81.6%;  Score 41.6;  DB 6;  Length 1353;
  Best Local Similarity   91.7%;  Pred. No. 0.036;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||||
Db        892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939


RESULT 14
AR270618
LOCUS       AR270618               2072 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1181 from patent US 6500938.
ACCESSION   AR270618
VERSION     AR270618.1  GI:29701852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2072)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1181 31-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .2072
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           81.6%;  Score 41.6;  DB 6;  Length 2072;
  Best Local Similarity   91.7%;  Pred. No. 0.035;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||||
Db       1304 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351


RESULT 15
HUMADRA2RA
LOCUS       HUMADRA2RA             2072 bp    DNA     linear   PRI 30-OCT-1994
DEFINITION  Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION   M34041
VERSION     M34041.1  GI:178197
KEYWORDS    alpha-2-adrenergic receptor; plasma membrane protein;
            receptor-coupled G protein.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2072)
  AUTHORS   Lomasney,J.W., Lorenz,W., Allen,L.F., King,K., Regan,J.W.,
            Yang-Feng,T.L., Caron,M.G. and Lefkowitz,R.J.
  TITLE     Expansion of the alpha 2-adrenergic receptor family: cloning and
            characterization of a human alpha 2-adrenergic receptor subtype,
            the gene for which is located on chromosome 2
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
  MEDLINE   90311349
   PUBMED   2164221
COMMENT     Original source text: Human placenta DNA, clone alpha-2 C2.
            Draft entry and computer-readable sequence for [1] kindly submitted
            by J.W.Lomasney, 03-MAY-1990, for release after publication.
FEATURES             Location/Qualifiers
     source          1. .2072
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /map="2"
     gene            413. .1765
                     /gene="ADRA2B"
     CDS             413. .1765
                     /gene="ADRA2B"
                     /note="alpha-2-adrenergic receptor (alpha-2 C2)  old gene
                     name 'ADRA2RL1'"
                     /codon_start=1
                     /protein_id="AAA51666.1"
                     /db_xref="GI:178198"
                     /db_xref="GDB:G00-120-539"
                     /translation="MDHQDPYSVQATAAIAAAITFLILFTIFGNALVILAVLTSRSLR
                     APQNLFLVSLAAADILVATLIIPFSLANELLGYWYFRRTWCEVYLALDVLFCTSSIVH
                     LCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLIAAVISLPPLIYKGDQGPQPRG
                     RPQCKLNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSNRRGPRAKGGPGQGES
                     KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
                     LPNSGQGQKEGVCGASPEDEAEEEEEEEEEEECEPQAVPVSPASACSPPLQQPQGSR
                     VLATLRGQVLLGRGVGAIGGQWWRRRAHVTREKRFTFVLAVVIGVFVLCWFPFFFSYS
                     LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                     "
ORIGIN      Chromosome 2.

  Query Match           81.6%;  Score 41.6;  DB 9;  Length 2072;
  Best Local Similarity   91.7%;  Pred. No. 0.035;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||||
Db       1304 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351


Search completed: March  2, 2004, 06:08:06
Job time : 865.5 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 04:46:17 ; Search time 267.5 Seconds
(without alignments)
809.937 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	828	9	ADB59041	Adb59041 Toxicity-
	2	51	100.0	1344	4	AAI99906	Aai99906 Human alp
	3	47.8	93.7	1344	5	AAD04761	Aad04761 Human alp
	4	47.8	93.7	1344	6	AAD44388	Aad44388 Human alp
	5	41.8	82.0	6904	6	ABL32074	Abl32074 Human imm
	6	41.8	82.0	6904	6	AAD28364	Aad28364 Human che
	7	41.6	81.6	1353	4	AAI99905	Aai99905 Human alp
	8	41.6	81.6	1353	5	AAD04762	Aad04762 Human alp
	9	41.6	81.6	1353	6	AAD44389	Aad44389 Human alp
	10	41.6	81.6	2064	2	AAQ14151	Aaq14151 Human alp
	11	41.6	81.6	2064	2	AAT59499	Aat59499 Human alp
	12	41.6	81.6	2072	7	ACA56583	Aca56583 Human sig
	13	41.6	81.6	3274	7	ABZ42624	Abz42624 Human alp
	14	36.6	71.8	593	4	AAD06932	Aad06932 3' end of
	15	36	70.6	2367	7	ABT20256	Abt20256 Aspergill
	16	36	70.6	2367	7	ABT20854	Abt20854 Aspergill
	17	36	70.6	4238	7	ABT17846	Abt17846 Aspergill
	18	36	70.6	4367	7	ABT19660	Abt19660 Aspergill
c	19	35	68.6	1429	3	AAC54146	Aac54146 Arabidops
	20	35	68.6	1820	2	AAQ88817	Aaq88817 Human sur
	21	34.4	67.5	392	6	ABN76609	Abn76609 Human ORF
	22	34.4	67.5	5000	2	AAV25477	Aav25477 Rat sulph
	23	34.4	67.5	5000	7	ABT41889	Abt41889 Toxicity
	24	34.4	67.5	6628	9	ADB58175	Adb58175 Toxicity-
	25	34.4	67.5	6628	9	ADB52677	Adb52677 Primary r
	26	34.2	67.1	5125	2	AAQ29703	Aaq29703 IRS-1. 3/
	27	33.8	66.3	291	5	AAS68926	Aas68926 DNA encod
	28	33.8	66.3	1018	7	ABZ24593	Abz24593 Mouse ova
	29	33.8	66.3	1019	3	AAD00296	Aad00296 Mouse ooc
	30	33.8	66.3	1481	3	AAD00297	Aad00297 Mouse ova
c	31	33.8	66.3	1721	6	ABQ76418	Abq76418 S. cerevi
	32	33.8	66.3	2629	9	ADD01220	Add01220 Human nuc
	33	33.8	66.3	6970	7	ABZ24594	Abz24594 Mouse ova
	34	33.4	65.5	2560	2	AAX18941	Aax18941 Human U62
	35	33.4	65.5	2981	9	ADB85264	Adb85264 Mouse RNA
	36	33.4	65.5	101786	3	AAF22293	Aaf22293 BAC conta
	37	33.2	65.1	193	4	AAI25502	Aai25502 Probe #15
	38	33.2	65.1	193	4	ABA71654	Aba71654 Human foe
	39	33.2	65.1	193	4	AAI51949	Aai51949 Probe #20
	40	33.2	65.1	193	4	ABA37774	Aba37774 Probe #16
	41	33.2	65.1	193	4	AAK46037	Aak46037 Human bon
	42	33.2	65.1	193	4	AAK19996	Aak19996 Human bra
	43	33.2	65.1	193	4	ABS45742	Abs45742 Human liv
	44	33.2	65.1	193	6	ABS20332	Abs20332 Human gen
c	45	33.2	65.1	324	2	AAV89689	Aav89689 EST clone

ALIGNMENTS

RESULT 1
ADB59041
ID ADB59041 standard; DNA; 828 BP.
XX
AC ADB59041;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 4067.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KW drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX
DR WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.
XX
PS Claim 1; SEQ ID NO 4067; 1156pp; English.
XX
CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect

CC of a compound, identifying an agent that modulates the onset or
CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 828 BP; 148 A; 271 C; 269 G; 140 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 9; Length 828;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 645

RESULT 2
AAI99906
ID AAI99906 standard; DNA; 1344 BP.
XX
AC AAI99906;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop variant encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1344
FT /*tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence is deleted for a 9 nucleotide
FT polymorphic site found at nucleotides 901-909 of the
FT wildtype alpha-2BAR protein (AAI99905)"
XX
PN WO200179561-A2.
XX
PD 25-OCT-2001.
XX
PF 17-APR-2001; 2001WO-US012575.
XX
PR 17-APR-2000; 2000US-00551744.
PR 10-AUG-2000; 2000US-00636259.
PR 19-OCT-2000; 2000US-00692077.
XX
PA (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
PI Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
DR P-PSDB; AAM52118.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting a
PT polymorphic site.
XX
PS Claim 5; Page 144-145; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a)
CC obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic
CC site comprising nucleotide positions 901-909 of (I), a site comprising
CC cytosine or guanine at position 753 of (IIV) or a site comprising (A)
CC (ggggcggggccg) or (B) (ggggcggctgag) at positions 961-972 of (III). The
CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
CC gene and further used to determine whether an individual is at increased
CC risk of developing a disease associated with alpha2B, alpha2A or alpha2,
CC comprising detecting a polymorphic site which correlate to disease
CC selected from cardiovascular disease, central nervous system disease and
CC combinations of these. In addition, the technique may be used to predict
CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
CC epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
CC UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine,
CC prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and
CC combinations of these) by detecting the polymorphic site and correlating
CC the site to a predetermined response (where the response is correlated to
CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
CC phosphate levels). The present sequence is that of the third
CC intracellular loop of the human alpha-2BAR variant, the sequence is
CC deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909
CC of the wildtype gene (AAI99905)
XX
SQ Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 4; Length 1344;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930

RESULT 3
AAD04761
ID AAD04761 standard; DNA; 1344 BP.
XX
AC AAD04761;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
XX
KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction; variant;
KW coronary artery; coronary heat disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1344
FT /*tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT variant protein"
XX
PN WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI000913.
XX
PR 22-OCT-1999; 99US-00422985.
XX
PA (JUVA-) JUVANTIA PHARMA LTD OY.
XX
PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssoenen K;
PI Salonen R, Kauhanen J, Valkonen V;
XX

```
DR   WPI; 2001-300318/31.
DR   P-PSDB; AAE00989.
XX
PT   New DNA molecule encoding variant specific adrenoceptor protein with
PT   deletion of specific amino acids located in the third intracellular loop
PT   of the polypeptide, for treating vascular contraction of coronary
PT   arteries.
XX
PS   Claim 3; Page 24-26; 37pp; English.
XX
CC   The present sequence is a gene encoding human alpha2B-adrenoceptor
CC   (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat
CC   element (amino acids 298-309) of 12 glutamates, in an acidic stretch of
CC   18 amino acids (amino acids 294-311), located in the third intracellular
CC   loop of the receptor polypeptide. The variant is obtained by deletion of
CC   three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR
CC   gene is located on chromosome 2. Alpha2-AR mediate many of the
CC   physiological effects of the catecholamines, norepinephrine and
CC   epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating
CC   a mammal suffering from vascular contraction of coronary arteries and a
CC   disease involving vascular contraction of coronary arteries which is
CC   clinically expressed as coronary heat disease (CHD), unstable chronic
CC   angina pectoris which is clinically expressed as Prinzmetal's variant
CC   form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
CC   gene therapy
XX
SQ   Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;

  Query Match             93.7%;  Score 47.8;  DB 5;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 0.00057;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 4
AAD44388
ID   AAD44388 standard; DNA; 1344 BP.
XX
AC   AAD44388;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Human alpha-2B-adrenoceptor variant DNA.
XX
KW   Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW   hypertension; hypotensive; variant; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1344
FT                   /*tag= a
FT                   /product= "Human alpha-2B-adrenoceptor variant protein"
XX
PN   WO200266617-A1.
XX
PD   29-AUG-2002.
XX
PF   13-FEB-2002; 2002WO-FI000113.
XX
PR   20-FEB-2001; 2001FI-00000323.
XX
PA   (JURI-) JURILAB LTD OY.
XX
PI   Salonen J;
XX
DR   WPI; 2002-667063/71.
DR   P-PSDB; AAE26633.
XX
PT   Detecting a risk of hypertension and targeting treatment in a subject by
PT   determining the pattern of alleles encoding a variant alpha-2-
PT   adrenoceptor.
XX
PS   Disclosure; Page 24-26; 35pp; English.
XX
CC   The invention relates to a method for detecting a risk of hypertension by
CC   determining the pattern of alleles encoding a variant alpha-2B-
CC   adrenoceptor (AR) protein. The methods and compositions of the invention
CC   are useful for detecting risks and targeting treatment for hypertension.
CC   The kit is also useful for selecting for clinical drug trials testing the
CC   antihypertensive effect of compounds. The present sequence is human alpha
CC   -2B-adrenoceptor variant DNA
XX
SQ   Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;

  Query Match             93.7%;  Score 47.8;  DB 6;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 0.00057;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 5
ABL32074
ID   ABL32074 standard; DNA; 6904 BP.
XX
AC   ABL32074;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 47.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007537.
XX
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful for
PT   diagnosis and treatment of diseases associated with abnormal cytosine
PT   methylation.
XX
PS   Claim 1; SEQ ID NO 47; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
```

```
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention
XX
SQ   Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 0 U; 1 Other;

  Query Match             82.0%;  Score 41.8;  DB 6;  Length 6904;
  Best Local Similarity   95.6%;  Pred. No. 0.025;
  Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              |||||||||| |||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 6
AAD28364
ID   AAD28364 standard; DNA; 6904 BP.
XX
AC   AAD28364;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human chemically treated genomic DNA #5.
XX
KW   Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive;
KW   adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism;
KW   behavioural disorder; neurological; psychiatric; cancer; schizophrenia;
KW   Tourette's syndrome; smoking; human immunodeficiency virus dementia;
KW   drug abuse; migraine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200202809-A2.
XX
PD   10-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP007540.
XX
PR   30-JUN-2000; 2000DE-01032529.
PR   01-SEP-2000; 2000DE-01043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-154759/20.
XX
PT   Novel nucleic acid useful for diagnosis and therapy of behavioral
PT   disorder, neurological disorder and cancer, comprises a sequence of a
PT   segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT   gene.
XX
PS   Claim 1; Page 40-44; 190pp; English.
XX
CC   The invention relates to nucleic acids comprising a segment of chemically
CC   pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC   relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC   useful for detecting cytosine methylations. The pretreated DNA is useful
CC   for the diagnosis or therapy of behavioural disorders, neurological
CC   disorders and cancer, in particular major depressive disorder, Tourette's
CC   syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC   drug abuse, alcoholism, personality traits, compulsive gambling, human
CC   immunodeficiency virus dementia, migraine, behaviours in schizophrenic
CC   and schizoaffective patients, and suicidal behaviour in patients with
CC   schizophrenia. The nucleic acid is useful for detecting the methylation
CC   state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC   (SNPs). The present sequence is human chemically treated genomic DNA
XX
SQ   Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 0 U; 1 Other;

  Query Match             82.0%;  Score 41.8;  DB 6;  Length 6904;
  Best Local Similarity   95.6%;  Pred. No. 0.025;
  Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              |||||||||| |||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 7
AAI99905
ID   AAI99905 standard; DNA; 1353 BP.
XX
AC   AAI99905;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Human alpha-2BAR third intracellular loop encoding DNA.
XX
KW   Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW   polymorphic site; allelic variant; cardiovascular disease;
KW   central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW   phosphorylation; inositol phosphate; alpha-2BAR;
KW   GenBank Accession AF009500; chromosome 2; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1353
FT                   /*tag=  a
FT                   /product= "alpha-2BAR"
FT                   /note= "sequence includes a 9 nucleotide polymorphic site
FT                   at nucleotides 901-909 absent in the alpha-2BAR variant
FT                   (AAI99906)"
XX
PN   WO200179561-A2.
XX
PD   25-OCT-2001.
XX
PF   17-APR-2001; 2001WO-US012575.
XX
PR   17-APR-2000; 2000US-00551744.
PR   10-AUG-2000; 2000US-00636259.
PR   19-OCT-2000; 2000US-00692077.
XX
PA   (LIGG/) LIGGETT S B.
PA   (SMAL/) SMALL K M.
XX
PI   Liggett SB,  Small KM;
XX
DR   WPI; 2001-611728/70.
DR   P-PSDB; AAM52117.
XX
PT   Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT   determining whether an individual is at increased risk of developing a
PT   disease associated with the corresponding receptor comprises detecting a
PT   polymorphic site.
XX
PS   Claim 4; Page 144; 163pp; English.
XX
CC   The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC   receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a)
CC   obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
CC   or alpha2C or fragment or complement of; and (b) detecting a polymorphic
CC   site comprising nucleotide positions 901-909 of (I), a site comprising
CC   cytosine or guanine at position 753 of (IIV) or a site comprising (A)
CC   (ggggcggggccg) or (B) (ggggcggctgag) at positions 961-972 of (III). The
CC   method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
CC   gene and further used to determine whether an individual is at increased
CC   risk of developing a disease associated with alpha2B, alpha2A or alpha2,
CC   comprising detecting a polymorphic site which correlate to disease
CC   selected from cardiovascular disease, central nervous system disease and
CC   combinations of these. In addition, the technique may be used to predict
CC   an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
CC   epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
CC   UK14304, BHT933 and combinations of these) or antagonist (e.g. yohimbine,
```

CC prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and
CC combinations of these) by detecting the polymorphic site and correlating
CC the site to a predetermined response (where the response is correlated to
CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
CC phosphate levels). The present sequence is that of the third
CC intracellular loop of the human alpha-2BAR (GenBank Accession AF009500),
CC the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-
CC 909, absent in the alpha-2BAR variant (AAI99906)
XX
SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 4; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.026;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 8
AAD04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heat disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1353
FT /*tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT protein"
XX
PN WO200129082-A1.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-FI000913.
XX
PR 22-OCT-1999; 99US-00422985.
XX
PA (JUVA-) JUVANTIA PHARMA LTD OY.
XX
PI Snapir A, Heinonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssoenen K;
PI Salonen R, Kauhanen J, Valkonen V;
XX
DR WPI; 2001-300318/31.
DR P-PSDB; AAE00990.
XX
PT New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular loop
PT of the polypeptide, for treating vascular contraction of coronary
PT arteries.
XX
PS Disclosure; Page 27-29; 37pp; English.
XX
CC The present sequence is a gene encoding human alpha2B-adrenoceptor
CC (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
CC (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
CC acids (amino acids 294-311), located in the third intracellular loop of
CC the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
CC Alpha2-AR mediate many of the physiological effects of the
CC catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-
CC adrenoceptor is useful for treating a mammal suffering from vascular
CC contraction of coronary arteries and a disease involving vascular
CC contraction of coronary arteries which is clinically expressed as
CC coronary heat disease (CHD), unstable chronic angina pectoris which is
CC clinically expressed as Prinzmetal's variant form or acute myocardial
CC infarction (AMI). Alpha2B-AR gene is used in gene therapy
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 5; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.026;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 9
AAD44389
ID AAD44389 standard; DNA; 1353 BP.
XX
AC AAD44389;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human alpha-2B-adrenoceptor gene.
XX
KW Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KW hypertension; hypotensive; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1353
FT /*tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"
XX
PN WO200266617-A1.
XX
PD 29-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-FI000113.
XX
PR 20-FEB-2001; 2001FI-00000323.
XX
PA (JURI-) JURILAB LTD OY.
XX
PI Salonen J;
XX
DR WPI; 2002-667063/71.
DR P-PSDB; AAE26634.
XX
PT Detecting a risk of hypertension and targeting treatment in a subject by
PT determining the pattern of alleles encoding a variant alpha-2-
PT adrenoceptor.
XX
PS Disclosure; Page 27-29; 35pp; English.
XX
CC The invention relates to a method for detecting a risk of hypertension by
CC determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing the
CC antihypertensive effect of compounds. The present sequence is human alpha
CC -2B-adrenoceptor gene
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 6; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.026;

```
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db        892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939


RESULT 10
AAQ14151
ID   AAQ14151 standard; DNA; 2064 BP.
XX
AC   AAQ14151;
XX
DT   06-JAN-1992  (first entry)
XX
DE   Human alpha 2 beta adrenergic receptor gene.
XX
KW   Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             288. .1752
FT                   /*tag=  a
XX
PN   US5053337-A.
XX
PD   01-OCT-1991.
XX
PF   30-OCT-1989;   89US-00428856.
XX
PR   30-OCT-1989;   89US-00428856.
XX
PA   (NEUR-) NEUROGENETIC CORP.
XX
PI   Weinshank RL;  Hartig PR;
XX
DR   WPI; 1991-310087/42.
DR   P-PSDB; AAR14149.
XX
PT   Isolated DNA encoding human adrenergic receptor - for detecting nucleic
PT   acids encoding alpha, 2-beta adrenergic receptor, for screening drugs.
XX
PS   Claim 1; Fig 2; 15pp; English.
XX
CC   Clone NGC-alpha2beta was isolated from a human spleen genomic library by
CC   screening with a fragment of the human 5-HT1A receptor gene. The gene can
CC   be used to express recombinant receptor protein which can be used to
CC   produce antibodies for inhibition of receptor function
XX
SQ   Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

  Query Match             81.6%;  Score 41.6;  DB 2;  Length 2064;
  Best Local Similarity   91.7%;  Pred. No. 0.027;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db       1290 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1337


RESULT 11
AAT59499
ID   AAT59499 standard; DNA; 2064 BP.
XX
AC   AAT59499;
XX
DT   25-MAR-2003  (revised)
DT   06-MAY-1997  (first entry)
XX
DE   Human alpha-2b adrenergic receptor genomic DNA clone.
XX
KW   Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine;
KW   signal transduction; neurotransmitter; ligand; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             288. .1751
FT                   /*tag=  a
XX
PN   US5595880-A.
XX
PD   21-JAN-1997.
XX
PF   22-OCT-1992;   92US-00965040.
XX
PR   30-OCT-1989;   89US-00428856.
PR   30-MAY-1991;   91US-00707604.
XX
PA   (SYNA-) SYNAPTIC PHARM CORP.
XX
PI   Hartig PR,  Weinshank RL;
XX
DR   WPI; 1997-107576/10.
DR   P-PSDB; AAW11804.
XX
PT   Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
PT   expressing recombinant receptor.
XX
PS   Disclosure; Fig 2A-E; 16pp; English.
XX
CC   A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic
CC   receptor (AAW11804), a member of the rhodopsin-like signal transducer
CC   family. It was isolated from a human spleen genomic library in the lambda
CC   vector Charon 28 by screening with a 1.6 kb fragment of the human 5-
CC   hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA
CC   encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors
CC   have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial,
CC   yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-
CC   2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in
CC   novel methods to identify drugs which specifically interact with, and
CC   bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

  Query Match             81.6%;  Score 41.6;  DB 2;  Length 2064;
  Best Local Similarity   91.7%;  Pred. No. 0.027;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || ||  |  ||||||||||||||||||||||||||||||||||||||||||
Db       1290 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1337


RESULT 12
ACA56583
ID   ACA56583 standard; cDNA; 2072 BP.
XX
AC   ACA56583;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1181.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
```

PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1181; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 7; Length 2072;
Best Local Similarity 91.7%; Pred. No. 0.027;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1304 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351

RESULT 13
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP.
XX
AC ABZ42624;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR P-PSDB; ABP81780.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;

Query Match 81.6%; Score 41.6; DB 7; Length 3274;
Best Local Similarity 91.7%; Pred. No. 0.028;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 14
AAD06932
ID AAD06932 standard; cDNA; 593 BP.
XX
AC AAD06932;
XX
DT 06-AUG-2001 (first entry)
XX
DE 3' end of human melanoma tumour-associated antigen cDNA from clone 5.31.
XX
KW Human; melanoma tumour-associated antigen; cytostatic; gene therapy;
KW vaccine; cancer; immune response; metastatic melanoma; immunotherapy; ss.
XX

OS Homo sapiens.
XX
PN WO200129064-A2.
XX
PD 26-APR-2001.
XX
PF 18-OCT-2000; 2000WO-US041260.
XX
PR 18-OCT-1999; 99US-0160042P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Strong TV, Conry RM, Lobuglio AF;
XX
DR WPI; 2001-308473/32.
XX
PT Isolated DNA sequence encoding a melanoma tumor associated antigen,
PT useful for detection, diagnosis and staging of melanomas, monitoring
PT metastatic melanomas and as a target for immunotherapy.
XX
PS Claim 1; Fig 2G; 55pp; English.
XX
CC The present sequence is 3' end cDNA of clone 5.31 encoding human melanoma
CC tumour-associated antigen. The cDNA is useful in gene therapy and as an
CC oligonucleotide probe for detecting mRNA coding for the melanoma tumour-
CC associated antigen in a sample. The cDNA is useful for vaccinating an
CC individual who is at risk of getting cancer, suspected of having cancer
CC or has cancer. The present sequence is useful for inhibiting growth of
CC melanoma tumour by inducing an immune response against it. The melanoma
CC tumour-associated antigen is useful for detection, diagnosis and staging
CC of melanoma, monitoring metastatic melanoma, as new targets for
CC immunotherapy. The identification of novel tumour antigens may allow
CC recurrence and metastatic disease to be detected and disease burden
CC monitored. Characterisation of the melanoma tumour-associated antigen is
CC of particular use in melanoma research
XX
SQ Sequence 593 BP; 158 A; 115 C; 146 G; 174 T; 0 U; 0 Other;

Query Match 71.8%; Score 36.6; DB 4; Length 593;
Best Local Similarity 82.4%; Pred. No. 0.56;
Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
||||| || | || |||||||| |||||||| ||||||| ||||||| |||
Db 295 GAGGAGGAGGAAGATGAGGAGGACGAGGAGGAAGAAGAGAGTGAACCTCAG 345

RESULT 15
ABT20256
ID ABT20256 standard; DNA; 2367 BP.
XX
AC ABT20256;
XX
DT 16-APR-2003 (first entry)
XX
DE Aspergillus fumigatus essential gene #2614.
XX
KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
KW cancer; contamination; biofilm; antibody; immune response; ds.
XX
OS Aspergillus fumigatus.
XX
PN WO200286090-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013142.
XX
PR 23-APR-2001; 2001US-0285697P.
PR 27-APR-2001; 2001US-0287066P.
PR 05-JUN-2001; 2001US-0295890P.
PR 09-JUL-2001; 2001US-0303899P.
PR 31-AUG-2001; 2001US-0316362P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
XX
DR WPI; 2003-093124/08.
XX
PT New purified or isolated nucleic acids of essential genes of Aspergillus
PT fumigatus, useful for treating or preventing infections by A. fumigatus,
PT or for treating a non-infectious disease in a subject e.g. cancer.
XX
PS Disclosure; Page; 175pp; English.
XX
CC The invention relates to novel purified or isolated nucleic acids of
CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of
CC the invention are used to treat or prevent infections by a pathogenic
CC organism such as A. fumigatus, to treat a non-infectious disease in a
CC subject (e.g. cancer), to prevent or contain contamination of an object
CC by A. fumigatus, or to prevent or inhibit formation on a surface of a
CC biofilm comprising A. fumigatus. The polynucleotides are useful for
CC expressing recombinant protein for characterisation, screening or
CC therapeutic use, as markers for host tissues in which the pathogenic
CC organisms invade or reside, for comparing with the DNA sequence of A.
CC fumigatus to identify duplicated genes or paralogues having the same or
CC similar biochemical activity and/or function, for comparing with DNA
CC sequences of other related or distant pathogenic organisms to identify
CC potential orthologous essential or virulence genes, for selecting and
CC making oligomers for attachment to a nucleic acid array for examination
CC of expression patterns, for raising anti-protein antibodies, as an
CC antigen to raise anti-DNA antibodies or to elicit another immune
CC response, and for identifying polynucleotides encoding the other protein
CC with which binding occurs or to identify inhibitors of the binding
CC interaction. The polypeptides may be used to raise antibodies or to
CC elicit immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as a marker for
CC host tissues in which pathogenic organism invade or reside, and to
CC isolate correlative receptors or ligands in the case or virulence
CC factors. This polynucleotide sequence represents one of the essential
CC genes of Aspergillus fumigatus of the invention
XX
SQ Sequence 2367 BP; 630 A; 644 C; 681 G; 412 T; 0 U; 0 Other;

Query Match 70.6%; Score 36; DB 7; Length 2367;
Best Local Similarity 88.6%; Pred. No. 0.87;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
||||| |||| |||||||||||||||| |||||||||| |||
Db 2314 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAAGAGGAAGAGTTTGA 2357

Search completed: March 2, 2004, 05:39:01
Job time : 268.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:39:14 ; Search time 60 Seconds
(without alignments)
471.708 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	41.6	81.6	2072	4	US-09-016-434-1181	Sequence 1181, Ap
	2	36.6	71.8	593	4	US-09-691-538A-12	Sequence 12, Appl
	3	35	68.6	1820	5	PCT-US94-09752-1	Sequence 1, Appli
	4	34.2	67.1	5125	1	US-08-094-948A-4	Sequence 4, Appli
	5	34.2	67.1	5125	5	PCT-US96-09319-4	Sequence 4, Appli
	6	33	64.7	650	3	US-09-328-111-333	Sequence 333, App
	7	32.8	64.3	404	4	US-09-621-976-18769	Sequence 18769, A
c	8	32.6	63.9	661	4	US-09-894-998A-34	Sequence 34, Appl
	9	32.2	63.1	2817	4	US-09-620-312D-1085	Sequence 1085, Ap
	10	32.2	63.1	14561	4	US-09-392-714-1	Sequence 1, Appli
	11	31.8	62.4	636	4	US-09-702-705-1668	Sequence 1668, Ap
	12	31.8	62.4	636	4	US-09-736-457-1668	Sequence 1668, Ap
	13	31.8	62.4	636	4	US-09-614-124B-1668	Sequence 1668, Ap
	14	31.8	62.4	636	4	US-09-671-325-1668	Sequence 1668, Ap
	15	31.6	62.0	258	4	US-09-345-882-21	Sequence 21, Appl
	16	31.6	62.0	3211	2	US-08-574-959A-8	Sequence 8, Appli
	17	31.6	62.0	3211	3	US-09-357-014-8	Sequence 8, Appli
	18	31.6	62.0	3901	2	US-08-574-959A-6	Sequence 6, Appli
	19	31.6	62.0	3901	3	US-09-357-014-6	Sequence 6, Appli
	20	31.6	62.0	4226	4	US-09-620-312D-480	Sequence 480, App
	21	31.6	62.0	6002	4	US-09-345-882-4	Sequence 4, Appli
	22	31.6	62.0	162450	4	US-09-345-882-1	Sequence 1, Appli
	23	31.4	61.6	2556	4	US-09-817-310-1	Sequence 1, Appli
c	24	31.2	61.2	129	4	US-09-702-705-309	Sequence 309, App
c	25	31.2	61.2	129	4	US-09-736-457-309	Sequence 309, App
c	26	31.2	61.2	129	4	US-09-614-124B-309	Sequence 309, App
c	27	31.2	61.2	129	4	US-09-671-325-309	Sequence 309, App
c	28	31.2	61.2	129	4	US-09-589-184-309	Sequence 309, App
	29	31.2	61.2	403	4	US-09-621-976-18731	Sequence 18731, A
	30	31.2	61.2	427	4	US-09-621-976-18711	Sequence 18711, A
	31	31.2	61.2	438	4	US-09-702-705-1028	Sequence 1028, Ap
	32	31.2	61.2	438	4	US-09-736-457-1028	Sequence 1028, Ap
	33	31.2	61.2	438	4	US-09-614-124B-1028	Sequence 1028, Ap
	34	31.2	61.2	438	4	US-09-671-325-1028	Sequence 1028, Ap
	35	31.2	61.2	450	4	US-09-621-976-3667	Sequence 3667, Ap
	36	31.2	61.2	452	4	US-09-621-976-3669	Sequence 3669, Ap
	37	31.2	61.2	458	4	US-09-621-976-1227	Sequence 1227, Ap
	38	31.2	61.2	459	4	US-09-621-976-1224	Sequence 1224, Ap
	39	31.2	61.2	464	4	US-09-621-976-1223	Sequence 1223, Ap
	40	31.2	61.2	464	4	US-09-621-976-3665	Sequence 3665, Ap
	41	31.2	61.2	464	4	US-09-621-976-18757	Sequence 18757, A
	42	31.2	61.2	476	4	US-09-621-976-18704	Sequence 18704, A
	43	31.2	61.2	514	4	US-09-621-976-3661	Sequence 3661, Ap
	44	31.2	61.2	521	4	US-09-621-976-18772	Sequence 18772, A
	45	31.2	61.2	686	4	US-09-166-350-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-016-434-1181
; Sequence 1181, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2072 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178197
US-09-016-434-1181

Query Match 81.6%; Score 41.6; DB 4; Length 2072;
Best Local Similarity 91.7%; Pred. No. 0.0014;

Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||
Db       1304 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351
```

RESULT 2
US-09-691-538A-12
; Sequence 12, Application US/09691538A
; Patent No. 6677444
; GENERAL INFORMATION:
; APPLICANT: Strong, Theresa
; APPLICANT: Conry, Robert M.
; APPLICANT: LoBuglio, Albert F.
; TITLE OF INVENTION: Melanoma Antigens and Methods of Use
; FILE REFERENCE: D6253
; CURRENT APPLICATION NUMBER: US/09/691,538A
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/160,042
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 12
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: 3' end of clone 5.31 encoding a melanoma
; OTHER INFORMATION: tumor-associated antigen
US-09-691-538A-12

Query Match 71.8%; Score 36.6; DB 4; Length 593;
Best Local Similarity 82.4%; Pred. No. 0.033;
Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||  ||  |  ||  |||||||| ||||||| |||||| ||||||| |||
Db        295 GAGGAGGAGGAAGATGAGGAGGACGAGGAGGAAGAAGAGAGTGAACCTCAG 345
```

RESULT 3
PCT-US94-09752-1
; Sequence 1, Application PC/TUS9409752
; GENERAL INFORMATION:
; APPLICANT: David S. Strayer and Avinash Chander
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Targeting Cells and Modulating Pulmonary Surfactant Secretion
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09752
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/176,218
; FILING DATE: December 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/114,951
; FILING DATE: August 31, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US94-09752-1

Query Match 68.6%; Score 35; DB 5; Length 1820;
Best Local Similarity 88.4%; Pred. No. 0.1;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTG 43
              || |||||  | |||||||||||||||||| ||||||||  ||||
Db        572 GAAGATGATGATGAAGAGGAGGAGGAGGAAGAGGAAGAATGTG 614
```

RESULT 4
US-08-094-948A-4
; Sequence 4, Application US/08094948A
; Patent No. 5621075
; GENERAL INFORMATION:
; APPLICANT: Kahn, C. Ronald
; APPLICANT: White, Morris F.
; APPLICANT: Rothenberg, Paul Louis
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/094,948A
; FILING DATE: 21-JULY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,982
; FILING DATE: 18-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis (PLM)
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-013DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5125 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 589..4053
US-08-094-948A-4

Query Match 67.1%; Score 34.2; DB 1; Length 5125;
Best Local Similarity 83.0%; Pred. No. 0.19;
Matches 39; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
Qy          3 GGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              ||| || || || |||||||||||| ||||||| ||| | |||||||
Db         53 GGAGGAGGCAGAGGAGGAGGAGGAGAAGGAGGAGGAGGGAGAACCCC 99


RESULT 5
PCT-US96-09319-4
; Sequence 4, Application PC/TUS9609319
;  GENERAL INFORMATION:
;    APPLICANT:  Kahn, C. Ronald
;    APPLICANT:  White, Morris F.
;    APPLICANT:  Rothenberg, Paul Louis
;    TITLE OF INVENTION:  INSULIN RECEPTOR SUBSTRATE
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lahive & Cockfield
;      STREET:  60 State Street, Suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09319
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/094,948
;      FILING DATE:  21-JULY-1993
;      APPLICATION NUMBER:  US 07/643,982
;      FILING DATE:  18-JAN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Myers, Louis (PLM)
;      REGISTRATION NUMBER:  35,965
;      REFERENCE/DOCKET NUMBER:  JDP-013DV
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5125 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  589..4053
PCT-US96-09319-4

  Query Match             67.1%;  Score 34.2;  DB 5;  Length 5125;
  Best Local Similarity   83.0%;  Pred. No. 0.19;
  Matches   39;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          3 GGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              ||| || || || |||||||||||| ||||||| ||| | |||||||
Db         53 GGAGGAGGCAGAGGAGGAGGAGGAGAAGGAGGAGGAGGGAGAACCCC 99


RESULT 6
US-09-328-111-333
; Sequence 333, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
;  APPLICANT: Endege, Wilson O.
;  APPLICANT: Steinmann, Kathleen E.
;  APPLICANT: Astle, Jon H.
;  APPLICANT: Burgess, Christopher C.
;  APPLICANT: Bushnell, Steven E.
;  APPLICANT: Carroll III, Eddie
;  APPLICANT: Catino, Theodore J.
;  APPLICANT: Derti, Adnan
;  APPLICANT: Ford, Donna M.
;  APPLICANT: Lewis, Marcia E.
;  APPLICANT: Monahan, John E.
;  APPLICANT: Schlegel, Robert
;  TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;  TITLE OF INVENTION: PRODUCTS
;  FILE REFERENCE: CCD-257 (US)
;  CURRENT APPLICATION NUMBER: US/09/328,111
;  CURRENT FILING DATE: 1999-06-08
;  EARLIER APPLICATION NUMBER: US 60/088,801
;  EARLIER FILING DATE: 1998-06-10
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 650
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(650)
;   OTHER INFORMATION: n = A,T,C or G
US-09-328-111-333

  Query Match             64.7%;  Score 33;  DB 3;  Length 650;
  Best Local Similarity   79.6%;  Pred. No. 0.34;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              ||||| ||||  ||||| |||||||||||||||||| |||   ||| | |
Db        245 GAGGAGGAAGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAAGAAACAC 293


RESULT 7
US-09-621-976-18769
; Sequence 18769, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 18769
;   LENGTH: 404
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-18769

  Query Match             64.3%;  Score 32.8;  DB 4;  Length 404;
  Best Local Similarity   84.1%;  Pred. No. 0.37;
  Matches   37;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              ||||| |||| ||  ||||| |||||||||||| ||||| |||||
Db        348 GAGGAAGAAGGTGGGGAGGAAGAGGAGGAGGAAGAAGAATGTGA 391


RESULT 8
US-09-894-998A-34/c
; Sequence 34, Application US/09894998A
; Patent No. 6537555
; GENERAL INFORMATION:
;  APPLICANT: Hosken, Nancy Ann
;  APPLICANT:  Craig H. Day
;  APPLICANT:  Davin C. Dillon
;  APPLICANT:  McGowan, Patrick
;  APPLICANT:  Sleath, Paul R.
```

```
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;  TITLE OF INVENTION:  TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;  FILE REFERENCE: 210121.538
;  CURRENT APPLICATION NUMBER: US/09/894,998A
;  CURRENT FILING DATE:  2001-06-28
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 661
;   TYPE: DNA
;   ORGANISM: HSV-2
US-09-894-998A-34

  Query Match             63.9%;  Score 32.6;  DB 4;  Length 661;
  Best Local Similarity   89.7%;  Pred. No. 0.44;
  Matches   35;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAG 39
              ||||| || || |||||||||||||||||||| |||||||
Db         42 GAGGAGGAGGCGGAAGAGGAGGAGGAGGAGGCGGAAGAG 4


RESULT 9
US-09-620-312D-1085
; Sequence 1085, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Rén, Feiyan
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  John Tillinghast
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1085
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (109)..(2817)
US-09-620-312D-1085

  Query Match             63.1%;  Score 32.2;  DB 4;  Length 2817;
  Best Local Similarity   82.2%;  Pred. No. 0.65;
  Matches   37;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAAC 46
              ||| ||| |  |||||||||||||| ||||||||||||  ||| |
Db        209 AGGGTGAGGAGGAAGAGGAGGAGGAAGAGGAGGAAGAGGATGACC 253


RESULT 10
US-09-392-714-1
; Sequence 1, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew J.
;  APPLICANT: Gure, Ali O.
;  APPLICANT: Williamson, Barbara
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd J.
;  TITLE OF INVENTION: Cancer Associated Antigens and Uses
;  TITLE OF INVENTION: Therefor
;  FILE REFERENCE: L0461/7062
;  CURRENT APPLICATION NUMBER: US/09/392,714A
;  CURRENT FILING DATE: 1999-09-09
;  EARLIER APPLICATION NUMBER: PCT/US98/14679
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 14561
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-392-714-1

  Query Match             63.1%;  Score 32.2;  DB 4;  Length 14561;
  Best Local Similarity   82.2%;  Pred. No. 0.75;
  Matches   37;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||| || |  || |||||||| |||||||| |||||| |||||
Db       6252 GAGGAGGAGGAAGATGAGGAGGACGAGGAGGAAGAAGAGAGTGAA 6296


RESULT 11
US-09-702-705-1668
; Sequence 1668, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-702-705-1668

  Query Match             62.4%;  Score 31.8;  DB 4;  Length 636;
  Best Local Similarity   76.5%;  Pred. No. 0.74;
  Matches   39;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| ||||  || ||||||||||||||||||| || |    || | ||
Db        586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636


RESULT 12
US-09-736-457-1668
; Sequence 1668, Application US/09736457
```

```
; Patent No. 6509448
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-736-457-1668

  Query Match             62.4%;  Score 31.8;  DB 4;  Length 636;
  Best Local Similarity   76.5%;  Pred. No. 0.74;
  Matches   39;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| ||||  || ||||||||||||||||||||| || |    || | ||
Db        586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636


RESULT 13
US-09-614-124B-1668
; Sequence 1668, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C9
;  CURRENT APPLICATION NUMBER: US/09/614,124B
;  CURRENT FILING DATE:  2001-07-11
;  NUMBER OF SEQ ID NOS: 1668
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-614-124B-1668

  Query Match             62.4%;  Score 31.8;  DB 4;  Length 636;
  Best Local Similarity   76.5%;  Pred. No. 0.74;
  Matches   39;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| ||||  || ||||||||||||||||||||| || |    || | ||
Db        586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636


RESULT 14
US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C12
;  CURRENT APPLICATION NUMBER: US/09/671,325
;  CURRENT FILING DATE:  2000-09-26
;  NUMBER OF SEQ ID NOS:  1825
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 636
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-671-325-1668

  Query Match             62.4%;  Score 31.8;  DB 4;  Length 636;
  Best Local Similarity   76.5%;  Pred. No. 0.74;
  Matches   39;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| ||||  || ||||||||||||||||||||| || |    || | ||
Db        586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636


RESULT 15
US-09-345-882-21
; Sequence 21, Application US/09345882
; Patent No. 6399373
; GENERAL INFORMATION:
;  APPLICANT: Bouguleret, Lydie
;  TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
;  TITLE OF INVENTION:  AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
;  FILE REFERENCE: GENSET.031A
;  CURRENT APPLICATION NUMBER: US/09/345,882
;  CURRENT FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER: US 60/091,315
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 60/111,909
;  PRIOR FILING DATE: 1998-12-10
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: Patent.pm
; SEQ ID NO 21
;   LENGTH: 258
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-345-882-21

  Query Match             62.0%;  Score 31.6;  DB 4;  Length 258;
  Best Local Similarity   89.5%;  Pred. No. 0.77;
  Matches   34;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGA 38
              || || ||||| |||||||||||||||||||| |||||
Db         32 GATGAAGAAGCAGAAGAGGAGGAGGAGGAGGAAGAAGA 69


Search completed: March  2, 2004, 08:36:49
Job time : 60 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 10:12:50 ; Search time 140 Seconds
(without alignments)
1314.149 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	1344	14	US-10-001-073-2	Sequence 2, Appli
2	47.8	93.7	1344	9	US-09-825-923-1	Sequence 1, Appli
3	47.8	93.7	1344	14	US-10-077-870-1	Sequence 1, Appli
4	41.8	82.0	6904	14	US-10-311-455-47	Sequence 47, Appl
5	41.6	81.6	1353	9	US-09-825-923-3	Sequence 3, Appli
6	41.6	81.6	1353	14	US-10-077-870-3	Sequence 3, Appli
7	41.6	81.6	1353	14	US-10-001-073-1	Sequence 1, Appli
8	41.6	81.6	2072	15	US-10-305-720-1181	Sequence 1181, Ap
9	41.6	81.6	3274	14	US-10-225-567A-41	Sequence 41, Appl
10	36	70.6	2367	14	US-10-128-714-6204	Sequence 6204, Ap
11	36	70.6	2367	14	US-10-128-714-7204	Sequence 7204, Ap
12	36	70.6	4238	14	US-10-128-714-204	Sequence 204, App
13	36	70.6	4367	14	US-10-128-714-5204	Sequence 5204, Ap
14	35.6	69.8	1012	12	US-10-424-599-139707	Sequence 139707,
15	34.8	68.2	1554	12	US-10-424-599-94653	Sequence 94653, A
16	34.4	67.5	392	11	US-09-864-408A-3111	Sequence 3111, Ap
17	34.4	67.5	6628	15	US-10-191-803-61	Sequence 61, Appl
18	33.8	66.3	182	9	US-09-844-864-12	Sequence 12, Appl
19	33.8	66.3	1018	9	US-09-844-864-5	Sequence 5, Appli
20	33.8	66.3	2526	12	US-10-424-599-108927	Sequence 108927,
21	33.8	66.3	3401	15	US-10-369-493-27799	Sequence 27799, A
22	33.4	65.5	2981	14	US-10-205-194-145	Sequence 145, App
23	33.2	65.1	193	9	US-09-864-761-23094	Sequence 23094, A
24	33.2	65.1	477	10	US-09-918-995-27029	Sequence 27029, A
25	33.2	65.1	492	9	US-09-864-761-6378	Sequence 6378, Ap
c 26	33	64.7	390	15	US-10-242-535A-43536	Sequence 43536, A
27	33	64.7	650	9	US-09-879-536-333	Sequence 333, App
28	33	64.7	1634	12	US-10-424-599-60174	Sequence 60174, A
29	32.8	64.3	150	14	US-10-029-386-18468	Sequence 18468, A
30	32.8	64.3	223	9	US-09-728-444-146	Sequence 146, App
31	32.8	64.3	253	9	US-09-728-445-59	Sequence 59, Appl
32	32.8	64.3	333	14	US-10-029-386-13715	Sequence 13715, A
33	32.8	64.3	336	15	US-10-085-117-303	Sequence 303, App
34	32.8	64.3	410	9	US-09-960-352-13656	Sequence 13656, A
35	32.8	64.3	525	14	US-10-029-386-4712	Sequence 4712, Ap
c 36	32.8	64.3	583	15	US-10-027-632-104255	Sequence 104255,
c 37	32.8	64.3	583	15	US-10-027-632-325232	Sequence 325232,
38	32.8	64.3	585	14	US-10-029-386-8	Sequence 8, Appli
39	32.8	64.3	1191	15	US-10-085-117-302	Sequence 302, App
40	32.8	64.3	1760	12	US-10-221-625-169	Sequence 169, App
c 41	32.8	64.3	1845	14	US-10-029-386-24791	Sequence 24791, A
42	32.8	64.3	2436	15	US-10-320-797-2316	Sequence 2316, Ap
43	32.8	64.3	3346	15	US-10-320-797-1316	Sequence 1316, Ap
44	32.8	64.3	5346	15	US-10-320-797-316	Sequence 316, App
c 45	32.8	64.3	5387	13	US-10-001-873-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-001-073-2
; Sequence 2, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-2

Query Match 100.0%; Score 51; DB 14; Length 1344;
Best Local Similarity 100.0%; Pred. No. 9.9e-07;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930
```

RESULT 2
US-09-825-923-1
; Sequence 1, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku

```
  ; APPLICANT:  Pesonen, Ullamari
  ; APPLICANT:  Scheinin, Mika
  ; APPLICANT:  Salonen, Jukka T
  ; APPLICANT:  Tuomainen, Tomi-Pekka
  ; APPLICANT:  Lakka, Timo A
  ; APPLICANT:  Nyyss"nen, Kristiina
  ; APPLICANT:  Salonen, Riitta
  ; APPLICANT:  Kauhanen, Jussi
  ; APPLICANT:  Valkonen, Veli-Pekka
  ; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
  ; TITLE OF INVENTION:  protein, and uses thereof
  ; FILE REFERENCE: Alpha-2B-AR variant
  ; CURRENT APPLICATION NUMBER: US/09/825,923
  ; CURRENT FILING DATE:  2001-04-05
  ; PRIOR APPLICATION NUMBER: 09/422,985
  ; PRIOR FILING DATE: 2000-05-25
  ; NUMBER OF SEQ ID NOS: 10
  ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
  ;   LENGTH: 1344
  ;   TYPE: DNA
  ;   ORGANISM: Homo sapiens
  ;   FEATURE:
  ;   NAME/KEY: CDS
  ;   LOCATION: (1)..(1341)
  ;   OTHER INFORMATION: Coding sequence for variant human
  ;   OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

  Query Match             93.7%;  Score 47.8;  DB 9;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 9.5e-06;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 3
US-10-077-870-1
; Sequence 1, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
;  APPLICANT: Salonen, Jukka T
;  TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
;  FILE REFERENCE: 0933-0183P
;  CURRENT APPLICATION NUMBER: US/10/077,870
;  CURRENT FILING DATE:  2002-05-21
;  PRIOR APPLICATION NUMBER: FI 20010323
;  PRIOR FILING DATE: 2001-02-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1341)
;   OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

  Query Match             93.7%;  Score 47.8;  DB 14;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 9.5e-06;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 4
US-10-311-455-47
```

```
; Sequence 47, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 47
;   LENGTH: 6904
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 6084
;   OTHER INFORMATION: n is a or g or c or t
US-10-311-455-47

  Query Match             82.0%;  Score 41.8;  DB 14;  Length 6904;
  Best Local Similarity   95.6%;  Pred. No. 0.00064;
  Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              |||||||||| ||||||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 5
US-09-825-923-3
; Sequence 3, Application US/09825923
; Patent No. US20010016338A1
; GENERAL INFORMATION:
;  APPLICANT: Snapir, Amir
;  APPLICANT:  Heinonen, Paula
;  APPLICANT:  Alhopuro, Pia
;  APPLICANT:  Karvonen, Matti
;  APPLICANT:  Koulu, Markku
;  APPLICANT:  Pesonen, Ullamari
;  APPLICANT:  Scheinin, Mika
;  APPLICANT:  Salonen, Jukka T
;  APPLICANT:  Tuomainen, Tomi-Pekka
;  APPLICANT:  Lakka, Timo A
;  APPLICANT:  Nyyss"nen, Kristiina
;  APPLICANT:  Salonen, Riitta
;  APPLICANT:  Kauhanen, Jussi
;  APPLICANT:  Valkonen, Veli-Pekka
;  TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
;  TITLE OF INVENTION:  protein, and uses thereof
;  FILE REFERENCE: Alpha-2B-AR variant
;  CURRENT APPLICATION NUMBER: US/09/825,923
;  CURRENT FILING DATE:  2001-04-05
;  PRIOR APPLICATION NUMBER: 09/422,985
;  PRIOR FILING DATE: 2000-05-25
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1353
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
```

; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
; OTHER INFORMATION: protein
US-09-825-923-3

Query Match 81.6%; Score 41.6; DB 9; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.00075;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 6
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
US-10-077-870-3

Query Match 81.6%; Score 41.6; DB 14; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.00075;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 7
US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073-1

Query Match 81.6%; Score 41.6; DB 14; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.00075;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 8
US-10-305-720-1181
; Sequence 1181, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressior
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1181
; LENGTH: 2072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181

Query Match 81.6%; Score 41.6; DB 15; Length 2072;
Best Local Similarity 91.7%; Pred. No. 0.00074;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||
Db 1304 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 1351

RESULT 9
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-41

Query Match 81.6%; Score 41.6; DB 14; Length 3274;
Best Local Similarity 91.7%; Pred. No. 0.00074;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
|| || | ||||||||||||||||||||||||||||||||||||||||||||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939

RESULT 10
US-10-128-714-6204
; Sequence 6204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi

; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6204
; LENGTH: 2367
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-6204

Query Match 70.6%; Score 36; DB 14; Length 2367;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
||||| |||| |||||||||||||||| |||||||||| |||
Db 2314 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAAGAGTTTGA 2357

RESULT 11
US-10-128-714-7204
; Sequence 7204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7204
; LENGTH: 2367
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-7204

Query Match 70.6%; Score 36; DB 14; Length 2367;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
||||| |||| |||||||||||||||| |||||||||| |||
Db 2314 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAAGAGTTTGA 2357

RESULT 12
US-10-128-714-204
; Sequence 204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 4238
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-204

Query Match 70.6%; Score 36; DB 14; Length 4238;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
||||| |||| |||||||||||||||| |||||||||| |||
Db 3314 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAAGAGTTTGA 3357

RESULT 13
US-10-128-714-5204
; Sequence 5204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5204
; LENGTH: 4367
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-5204

Query Match 70.6%; Score 36; DB 14; Length 4367;
Best Local Similarity 88.6%; Pred. No. 0.038;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
||||| |||| |||||||||||||||| |||||||||| |||
Db 3314 GAGGAGGAAGAAGAAGAGGAGGAGGAGGAAGAGGAAGAGTTTGA 3357

RESULT 14
US-10-424-599-139707
; Sequence 139707, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 139707
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97163C.1
US-10-424-599-139707

Query Match 69.8%; Score 35.6; DB 12; Length 1012;
Best Local Similarity 82.0%; Pred. No. 0.051;
Matches 41; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA 50
|| || || | |||||||||||||||||||||||||| |||| | |
Db 467 GAAGAAGACGTAGAAGAGGAGGAGGAGGAGGAAGAGTTTGAAGACGA 516

RESULT 15
US-10-424-599-94653
; Sequence 94653, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 94653
; LENGTH: 1554
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56483C.1
US-10-424-599-94653

Query Match 68.2%; Score 34.8; DB 12; Length 1554;
Best Local Similarity 84.8%; Pred. No. 0.089;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAAC 46
|||||||| | ||| |||||||||||||||||||| | || ||| |
Db 583 GAGGATGAGGATGATGAGGAGGAGGAGGAGGAGGATGTGTTTGACC 628

Search completed: March 2, 2004, 12:03:39
Job time : 141 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 07:20:29 ; Search time 2886 Seconds
(without alignments)
621.792 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq:*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq:*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq:*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq:*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq:*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq:*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq:*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq:*
16: /cgn2_6/ptodata/2/pna/US092A_COMB.seq:*
17: /cgn2_6/ptodata/2/pna/US092B_COMB.seq:*
18: /cgn2_6/ptodata/2/pna/US093A_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US093B_COMB.seq:*
20: /cgn2_6/ptodata/2/pna/US094_COMB.seq:*
21: /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
22: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
23: /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*
24: /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*
25: /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*
26: /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
27: /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*
28: /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*
29: /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*
30: /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*
31: /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*
32: /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*
33: /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*
34: /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*
35: /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*
36: /cgn2_6/ptodata/2/pna/US098D_COMB.seq:*
37: /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*
38: /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*
39: /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*
40: /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*
41: /cgn2_6/ptodata/2/pna/US099E_COMB.seq:*
42: /cgn2_6/ptodata/2/pna/US099F_COMB.seq:*
43: /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*
44: /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*
48: /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
49: /cgn2_6/ptodata/2/pna/US103A_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US103B_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US104A_COMB.seq:*
52: /cgn2_6/ptodata/2/pna/US104B_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US106_COMB.seq:*
54: /cgn2_6/ptodata/2/pna/US107A_COMB.seq:*
55: /cgn2_6/ptodata/2/pna/US107B_COMB.seq:*
56: /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
57: /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
58: /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
60: /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
61: /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
62: /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
63: /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
64: /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
65: /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
66: /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
67: /cgn2_6/ptodata/2/pna/US6011_COMB.seq:*
68: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
69: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
70: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
71: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
72: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
73: /cgn2_6/ptodata/2/pna/US6017_COMB.seq:*
74: /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
75: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
76: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
77: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
78: /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
79: /cgn2_6/ptodata/2/pna/US6023A_COMB.seq:*
80: /cgn2_6/ptodata/2/pna/US6023B_COMB.seq:*
81: /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
82: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
83: /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
84: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
85: /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
86: /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
87: /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
88: /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
89: /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
90: /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
91: /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
92: /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
93: /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*
94: /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*
95: /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*
96: /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
97: /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*
98: /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*
99: /cgn2_6/ptodata/2/pna/US6042_COMB.seq:*
100: /cgn2_6/ptodata/2/pna/US6043_COMB.seq:*
101: /cgn2_6/ptodata/2/pna/US6044_COMB.seq:*
102: /cgn2_6/ptodata/2/pna/US6045_COMB.seq:*
103: /cgn2_6/ptodata/2/pna/US6046_COMB.seq:*
104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:*
105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:*
106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:*
107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:*
108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:*
109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:*
110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	828	1	PCT-US03-03194-4067	Sequence 4067, Ap
2	51	100.0	828	100	US-60-436-643-4067	Sequence 4067, Ap
3	51	100.0	828	103	US-60-468-720-1259	Sequence 1259, Ap
4	51	100.0	1344	29	US-09-692-077B-2	Sequence 2, Appli
5	51	100.0	1344	29	US-09-692-077D-2	Sequence 2, Appli
6	51	100.0	1344	43	US-10-001-073-2	Sequence 2, Appli
7	51	100.0	1344	43	US-10-001-073A-2	Sequence 2, Appli
8	49	96.1	60	29	US-09-692-077D-25	Sequence 25, Appl
9	49	96.1	60	43	US-10-001-073A-55	Sequence 55, Appl
10	47.8	93.7	1344	20	US-09-422-985-1	Sequence 1, Appli
11	47.8	93.7	1344	33	US-09-825-923-1	Sequence 1, Appli
12	47.8	93.7	1344	44	US-10-077-870-1	Sequence 1, Appli
13	41.8	82.0	6904	49	US-10-311-455-47	Sequence 47, Appl
c 14	41.6	81.6	481	72	US-60-164-763-274	Sequence 274, App
c 15	41.6	81.6	481	72	US-60-169-842-1935	Sequence 1935, Ap
c 16	41.6	81.6	481	73	US-60-170-346-61	Sequence 61, Appl
17	41.6	81.6	516	31	US-09-726-174-3537	Sequence 3537, Ap
18	41.6	81.6	569	72	US-60-160-189-1492	Sequence 1492, Ap
19	41.6	81.6	569	72	US-60-160-190-231	Sequence 231, App
20	41.6	81.6	569	72	US-60-160-202-659	Sequence 659, App
21	41.6	81.6	569	72	US-60-169-840-3708	Sequence 3708, Ap
22	41.6	81.6	569	72	US-60-169-841-1172	Sequence 1172, Ap
23	41.6	81.6	569	72	US-60-169-842-2193	Sequence 2193, Ap
24	41.6	81.6	569	72	US-60-169-867-3351	Sequence 3351, Ap
c 25	41.6	81.6	601	39	US-09-949-004-4865	Sequence 4865, Ap
26	41.6	81.6	1353	20	US-09-422-985-3	Sequence 3, Appli
27	41.6	81.6	1353	29	US-09-692-077B-1	Sequence 1, Appli
28	41.6	81.6	1353	29	US-09-692-077D-1	Sequence 1, Appli
29	41.6	81.6	1353	33	US-09-825-923-3	Sequence 3, Appli
30	41.6	81.6	1353	43	US-10-001-073-1	Sequence 1, Appli
31	41.6	81.6	1353	43	US-10-001-073A-1	Sequence 1, Appli
32	41.6	81.6	1353	44	US-10-077-870-3	Sequence 3, Appli
33	41.6	81.6	1353	46	US-10-170-235-40719	Sequence 40719, A
34	41.6	81.6	1353	102	US-60-453-050-6437	Sequence 6437, Ap
35	41.6	81.6	1353	102	US-60-453-135-6437	Sequence 6437, Ap
36	41.6	81.6	1353	103	US-60-466-412-6437	Sequence 6437, Ap
37	41.6	81.6	1825	39	US-09-949-004-175	Sequence 175, App
38	41.6	81.6	2072	49	US-10-305-720-1181	Sequence 1181, Ap
39	41.6	81.6	3274	47	US-10-225-567A-41	Sequence 41, Appl
40	41.6	81.6	3655	107	US-60-500-315-890	Sequence 890, App
41	41.6	81.6	3891	107	US-60-500-315-891	Sequence 891, App
42	41.6	81.6	4050	76	US-60-207-360-68	Sequence 68, Appl
43	41.6	81.6	4050	76	US-60-207-360-110	Sequence 110, App
44	41.6	81.6	4050	76	US-60-207-360-111	Sequence 111, App
45	41.6	81.6	4050	76	US-60-207-360-112	Sequence 112, App

ALIGNMENTS

```
RESULT 1
PCT-US03-03194-4067
; Sequence 4067, Application PC/TUS0303194
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
;  FILE REFERENCE: 44921-5038-01-WO
;  CURRENT APPLICATION NUMBER: PCT/US03/03194
;  CURRENT FILING DATE:  2003-01-31
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: US 60/331,273
;  PRIOR FILING DATE: 2001-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4295
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4067
;    LENGTH: 828
;    TYPE: DNA
;    ORGANISM: Rattus norvegicus
;    FEATURE:
;    OTHER INFORMATION: Genbank Accession No. S67316
PCT-US03-03194-4067

  Query Match             100.0%;  Score 51;  DB 1;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 645


RESULT 2
US-60-436-643-4067
; Sequence 4067, Application US/60436643
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
;  FILE REFERENCE: 44921-5038-P15
;  CURRENT APPLICATION NUMBER: US/60/436,643
;  CURRENT FILING DATE:  2002-12-30
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: US 60/331,273
;  PRIOR FILING DATE: 2001-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 4295
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4067
```

```
;   LENGTH: 828
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. S67316
US-60-436-643-4067

  Query Match             100.0%;  Score 51;  DB 100;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 645


RESULT 3
US-60-468-720-1259
; Sequence 1259, Application US/60468720
; GENERAL INFORMATION:
;  APPLICANT: Higgs, Brandon
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Mendrick, Donna
;  TITLE OF INVENTION: Nucleic Acid Detection Assay Control Genes
;  FILE REFERENCE: 44921-5124-P1
;  CURRENT APPLICATION NUMBER: US/60/468,720
;  CURRENT FILING DATE:  2003-05-06
;  PRIOR APPLICATION NUMBER: US 60/396,145
;  PRIOR FILING DATE: 2002-07-17
;  NUMBER OF SEQ ID NOS: 1347
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1259
;   LENGTH: 828
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. S67316
US-60-468-720-1259

  Query Match             100.0%;  Score 51;  DB 103;  Length 828;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 645


RESULT 4
US-09-692-077B-2
; Sequence 2, Application US/09692077B
; GENERAL INFORMATION:
;  APPLICANT: Liggett, Stephen
;  TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
;  FILE REFERENCE: Sequences 1-22
;  CURRENT APPLICATION NUMBER: US/09/692,077B
;  CURRENT FILING DATE:  2000-10-19
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-692-077B-2

  Query Match             100.0%;  Score 51;  DB 29;  Length 1344;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930


RESULT 5
US-09-692-077D-2
; Sequence 2, Application US/09692077D
; GENERAL INFORMATION:
;  APPLICANT: Liggett, Stephen
;  APPLICANT:  Small, Kersten M.
;  TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
;  FILE REFERENCE: 10738-43
;  CURRENT APPLICATION NUMBER: US/09/692,077D
;  CURRENT FILING DATE:  2000-10-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-692-077D-2

  Query Match             100.0%;  Score 51;  DB 29;  Length 1344;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930


RESULT 6
US-10-001-073-2
; Sequence 2, Application US/10001073
; GENERAL INFORMATION:
;  APPLICANT: Liggett, Stephen
;  APPLICANT:  Small, Kirsten
;  TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
;  FILE REFERENCE: 13073-PCT
;  CURRENT APPLICATION NUMBER: US/10/001,073
;  CURRENT FILING DATE:  2001-11-01
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-001-073-2

  Query Match             100.0%;  Score 51;  DB 43;  Length 1344;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930


RESULT 7
US-10-001-073A-2
; Sequence 2, Application US/10001073A
; GENERAL INFORMATION:
;  APPLICANT: Small, Kersten M.
;  APPLICANT:  Liggett, Stephen
;  TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
;  FILE REFERENCE: 10738-42
;  CURRENT APPLICATION NUMBER: US/10/001,073A
;  CURRENT FILING DATE:  2001-11-01
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 1344
;   TYPE: DNA
```

; ORGANISM: Homo sapiens
US-10-001-073A-2

Query Match 100.0%; Score 51; DB 43; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930
```

RESULT 8
US-09-692-077D-25
; Sequence 25, Application US/09692077D
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kersten M.
; TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-43
; CURRENT APPLICATION NUMBER: US/09/692,077D
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077D-25

Query Match 96.1%; Score 49; DB 29; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 60
```

RESULT 9
US-10-001-073A-55
; Sequence 55, Application US/10001073A
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M.
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-42
; CURRENT APPLICATION NUMBER: US/10/001,073A
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-001-073A-55

Query Match 96.1%; Score 49; DB 43; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 60
```

RESULT 10
US-09-422-985-1
; Sequence 1, Application US/09422985
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/422,985
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human
; OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-422-985-1

Query Match 93.7%; Score 47.8; DB 20; Length 1344;
Best Local Similarity 96.1%; Pred. No. 0.11;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||||||||| |||||||||| ||||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930
```

RESULT 11
US-09-825-923-1
; Sequence 1, Application US/09825923
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Alhopuro, Pia
; APPLICANT: Karvonen, Matti
; APPLICANT: Koulu, Markku
; APPLICANT: Pesonen, Ullamari
; APPLICANT: Scheinin, Mika
; APPLICANT: Salonen, Jukka T
; APPLICANT: Tuomainen, Tomi-Pekka
; APPLICANT: Lakka, Timo A
; APPLICANT: Nyyss"nen, Kristiina
; APPLICANT: Salonen, Riitta
; APPLICANT: Kauhanen, Jussi
; APPLICANT: Valkonen, Veli-Pekka
; TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
; TITLE OF INVENTION: protein, and uses thereof
; FILE REFERENCE: Alpha-2B-AR variant
; CURRENT APPLICATION NUMBER: US/09/825,923
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/422,985
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1341)
; OTHER INFORMATION: Coding sequence for variant human

```
;   OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-825-923-1

  Query Match             93.7%;  Score 47.8;  DB 33;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 0.11;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 12
US-10-077-870-1
; Sequence 1, Application US/10077870
; GENERAL INFORMATION:
;  APPLICANT: Salonen, Jukka T
;  TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
;  FILE REFERENCE: 0933-0183P
;  CURRENT APPLICATION NUMBER: US/10/077,870
;  CURRENT FILING DATE:  2002-05-21
;  PRIOR APPLICATION NUMBER: FI 20010323
;  PRIOR FILING DATE: 2001-02-20
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1
;   LENGTH: 1344
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1341)
;   OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1

  Query Match             93.7%;  Score 47.8;  DB 44;  Length 1344;
  Best Local Similarity   96.1%;  Pred. No. 0.11;
  Matches   49;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||||||||||||||||||||| |||||||||| ||||||||||||||
Db        880 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAACCCCAG 930


RESULT 13
US-10-311-455-47
; Sequence 47, Application US/10311455
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 47
;   LENGTH: 6904
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 6084
;   OTHER INFORMATION: n is a or g or c or t
US-10-311-455-47

  Query Match             82.0%;  Score 41.8;  DB 49;  Length 6904;
  Best Local Similarity   95.6%;  Pred. No. 2.6;
  Matches   43;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              |||||||||| |||||||||||||||||||||||||| ||||||
Db       5880 GAGGATGAAGTTGAAGAGGAGGAGGAGGAGGAGGAAGATTGTGAA 5924


RESULT 14
US-60-164-763-274/c
; Sequence 274, Application US/60164763
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
;  FILE REFERENCE: CL000140
;  CURRENT APPLICATION NUMBER: US/60/164,763
;  CURRENT FILING DATE: 1999-11-12
;  NUMBER OF SEQ ID NOS: 1154
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 274
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Human
US-60-164-763-274

  Query Match             81.6%;  Score 41.6;  DB 72;  Length 481;
  Best Local Similarity   91.7%;  Pred. No. 3.1;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||
Db        215 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 168


RESULT 15
US-60-169-842-1935/c
; Sequence 1935, Application US/60169842
; GENERAL INFORMATION:
;  APPLICANT: Bonazzi, Vivien
;  TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
;  TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEINS AND USES THEREOF
;  FILE REFERENCE: CL000162
;  CURRENT APPLICATION NUMBER: US/60/169,842
;  CURRENT FILING DATE: 1999-12-09
;  NUMBER OF SEQ ID NOS: 5232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1935
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Human
US-60-169-842-1935

  Query Match             81.6%;  Score 41.6;  DB 72;  Length 481;
  Best Local Similarity   91.7%;  Pred. No. 3.1;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || || |  ||||||||||||||||||||||||||||||||||||||||
Db        215 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 168


Search completed: March  2, 2004, 11:49:23
Job time : 2889 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 08:34:44 ; Search time 16.5 Seconds
(without alignments)
520.698 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 164199 seqs, 84230614 residues

Total number of hits satisfying chosen parameters: 328398

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	33.8	66.3	1721	6	US-10-451-467A-261	Sequence 261, App
c	2	32.6	63.9	430442	6	US-10-417-375A-128	Sequence 128, App
	3	32.2	63.1	1330	6	US-10-767-701-13517	Sequence 13517, A
	4	32.2	63.1	3994	1	PCT-US04-02188-20	Sequence 20, Appl
	5	32.2	63.1	3994	6	US-10-764-425-20	Sequence 20, Appl
	6	32.2	63.1	398800	1	PCT-US03-32805-1	Sequence 1, Appli
c	7	31.2	61.2	353	6	US-10-767-701-29063	Sequence 29063, A
	8	31.2	61.2	188053	6	US-10-417-375A-125	Sequence 125, App
c	9	31.2	61.2	209320	6	US-10-767-471-10681	Sequence 10681, A
c	10	31	60.8	650	6	US-10-767-701-26619	Sequence 26619, A
c	11	31	60.8	54303	6	US-10-417-375A-79	Sequence 79, Appl
	12	31	60.8	310122	6	US-10-417-375A-1	Sequence 1, Appli
c	13	30.6	60.0	940	6	US-10-767-701-15708	Sequence 15708, A
	14	30.6	60.0	34304	6	US-10-767-471-10555	Sequence 10555, A
	15	30.6	60.0	45980	6	US-10-642-946-6	Sequence 6, Appli
	16	30.6	60.0	54303	6	US-10-417-375A-79	Sequence 79, Appl
c	17	30.6	60.0	150085	6	US-10-417-375A-167	Sequence 167, App
	18	30.6	60.0	219715	6	US-10-417-375A-63	Sequence 63, Appl
	19	30	58.8	666	6	US-10-767-701-23701	Sequence 23701, A
c	20	30	58.8	310122	6	US-10-417-375A-1	Sequence 1, Appli
c	21	29.8	58.4	1001	6	US-10-772-716-7	Sequence 7, Appli
c	22	29.6	58.0	201	6	US-10-767-471-31476	Sequence 31476, A
	23	29.6	58.0	264	6	US-10-767-701-24209	Sequence 24209, A
c	24	29.6	58.0	497	6	US-10-767-701-2690	Sequence 2690, Ap
	25	29.6	58.0	1064	6	US-10-767-701-9500	Sequence 9500, Ap
	26	29.6	58.0	1932	1	PCT-US04-03417-73	Sequence 73, Appl
	27	29.6	58.0	1932	6	US-10-772-636-73	Sequence 73, Appl
c	28	29.6	58.0	2086	6	US-10-767-701-14827	Sequence 14827, A
c	29	29.6	58.0	803755	6	US-10-767-471-10700	Sequence 10700, A
c	30	29.4	57.6	678	6	US-10-767-701-1864	Sequence 1864, Ap
c	31	29.4	57.6	828	6	US-10-767-701-20232	Sequence 20232, A
c	32	29.4	57.6	1316	6	US-10-767-701-13537	Sequence 13537, A
	33	29.4	57.6	3643	1	PCT-US04-03417-39	Sequence 39, Appl
	34	29.4	57.6	3643	6	US-10-772-636-39	Sequence 39, Appl
c	35	29.4	57.6	46193	6	US-10-767-471-10632	Sequence 10632, A
c	36	29.4	57.6	66158	6	US-10-765-790-72	Sequence 72, Appl
c	37	29.4	57.6	765267	6	US-10-767-471-10616	Sequence 10616, A
c	38	29.2	57.3	1231	6	US-10-767-701-3854	Sequence 3854, Ap
c	39	29.2	57.3	1623	6	US-10-767-701-14185	Sequence 14185, A
	40	29	56.9	378	6	US-10-767-701-13518	Sequence 13518, A
	41	29	56.9	1205	6	US-10-767-701-10125	Sequence 10125, A
c	42	29	56.9	1242	6	US-10-767-701-11456	Sequence 11456, A
c	43	29	56.9	1687	6	US-10-767-701-13851	Sequence 13851, A
	44	29	56.9	111469	6	US-10-767-471-10820	Sequence 10820, A
c	45	29	56.9	1126118	6	US-10-767-471-10615	Sequence 10615, A

ALIGNMENTS

RESULT 1
US-10-451-467A-261/c
; Sequence 261, Application US/10451467A
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 261
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-261

Query Match 66.3%; Score 33.8; DB 6; Length 1721;
Best Local Similarity 84.4%; Pred. No. 0.057;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              || |||||||  ||||||||||||||||||||| |||   |||
Db        631 GAAGATGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAA 587
```

RESULT 2
US-10-417-375A-128/c
; Sequence 128, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128

; LENGTH: 430442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-417-375A-128

Query Match 63.9%; Score 32.6; DB 6; Length 430442;
Best Local Similarity 80.9%; Pred. No. 0.22;
Matches 38; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 ATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
Db 370265 AGGAAGATGAAGAGGAGGAGGAGGAAGATGAAGAAGATGAAGACCAG 370219

RESULT 3
US-10-767-701-13517
; Sequence 13517, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13517
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS447_1
US-10-767-701-13517

Query Match 63.1%; Score 32.2; DB 6; Length 1330;
Best Local Similarity 82.2%; Pred. No. 0.16;
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
Db 258 GAGGATGAAGATGGCGAGGAGGAGGAGGAGGAAGAAGAAGAAGAA 302

RESULT 4
PCT-US04-02188-20
; Sequence 20, Application PC/TUS0402188
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 3994
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-02188-20

Query Match 63.1%; Score 32.2; DB 1; Length 3994;
Best Local Similarity 82.2%; Pred. No. 0.18;
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
Db 926 GAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAAGAGGAAGAA 970

RESULT 5
US-10-764-425-20
; Sequence 20, Application US/10764425
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 3994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-425-20

Query Match 63.1%; Score 32.2; DB 6; Length 3994;
Best Local Similarity 82.2%; Pred. No. 0.18;
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
Db 926 GAGGAGGAAGAAGAAGAAGAGGAAGAGGAGGAGGAAGAGGAAGAA 970

RESULT 6
PCT-US03-32805-1
; Sequence 1, Application PC/TUS0332805
; GENERAL INFORMATION:
; APPLICANT: deCODE genetics ehf.
; APPLICANT: Helgadottir, Anna
; APPLICANT: Gulcher, Jeffrey R.
; APPLICANT: Manolescu, Andrei
; TITLE OF INVENTION: Susceptibility Gene for Myocardial
; TITLE OF INVENTION: Infarction
; FILE REFERENCE: 2345.2048002
; CURRENT APPLICATION NUMBER: PCT/US03/32805
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/419,432
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 398800
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70677)...(70776)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (154988)...(155087)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 248521
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (269991)...(270091)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (272544)...(272643)

```
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (279545)...(279644)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (300892)...(300991)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (327555)...(327654)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (332849)...(332948)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (341698)...(341698)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (345190)...(345289)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (350504)...(350603)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (391524)...(391623)
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (396625)...(396724)
;   OTHER INFORMATION: n = A,T, C or G
PCT-US03-32805-1

  Query Match             63.1%;  Score 32.2;  DB 1;  Length 398800;
  Best Local Similarity   82.2%;  Pred. No. 0.28;
  Matches   37;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              || || |||| ||||||||| ||||||||||||||||||    |||
Db      51865 GATGAGGAAGATGAAGAGGATGAGGAGGAGGAGGAAGATGAAGAA 51909


RESULT 7
US-10-767-701-29063/c
; Sequence 29063, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof For Plant Improvement
;  FILE REFERENCE: 38-21(53535)B
;  CURRENT APPLICATION NUMBER: US/10/767,701
;  CURRENT FILING DATE:  2004-01-29
;  NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 29063
;   LENGTH: 353
;   TYPE: DNA
;   ORGANISM: Sorghum bicolor
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 8548511
US-10-767-701-29063

  Query Match             61.2%;  Score 31.2;  DB 6;  Length 353;
  Best Local Similarity   81.8%;  Pred. No. 0.27;
  Matches   36;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              || | |||||  ||||||||| |||| |||||||||||| | ||
Db        257 GACGGTGAAGGCGAAGAGGAGCAGGATGAGGAGGAAGAGCGCGA 214


RESULT 8
US-10-417-375A-125
; Sequence 125, Application US/10417375A
; GENERAL INFORMATION:
;  APPLICANT: David W. Morris
;  APPLICANT:  Marc Malandro
;  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
;  FILE REFERENCE: 529452001600
;  CURRENT APPLICATION NUMBER: US/10/417,375A
;  CURRENT FILING DATE:  2003-04-15
;  NUMBER OF SEQ ID NOS: 176
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
;   LENGTH: 188053
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(188053)
;   OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-125

  Query Match             61.2%;  Score 31.2;  DB 6;  Length 188053;
  Best Local Similarity   81.8%;  Pred. No. 0.5;
  Matches   36;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              ||||| ||||  ||||||||| || |||||||||| ||| | ||
Db      63527 GAGGAGGAAGAAGAAGAGGAAGAAGAGGAGGAGGAGGAGGGGGA 63570


RESULT 9
US-10-767-471-10681/c
; Sequence 10681, Application US/10767471
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001505
;  CURRENT APPLICATION NUMBER: US/10/767,471
;  CURRENT FILING DATE:  2004-01-30
;  NUMBER OF SEQ ID NOS: 50231
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10681
;   LENGTH: 209320
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(209320)
;   OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2
US-10-767-471-10681

  Query Match             61.2%;  Score 31.2;  DB 6;  Length 209320;
  Best Local Similarity   81.8%;  Pred. No. 0.5;
  Matches   36;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              || || |||| |||||||||||||||| || ||||||  |||
Db      51530 GAAGAAGAAGAAGAAGAGGAGGAGGAGGAAGAAGAAGAGATTGA 51487


RESULT 10
US-10-767-701-26619/c
; Sequence 26619, Application US/10767701
; GENERAL INFORMATION:
;  APPLICANT: Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
```

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 26619
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30976844
US-10-767-701-26619

Query Match 60.8%; Score 31; DB 6; Length 650;
Best Local Similarity 87.2%; Pred. No. 0.32;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAG 39
|| || |||| ||||||||||||||||||||||| |||
Db 88 GAAGAAGAAGAGGAAGAGGAGGAGGAGGAGGAGGAGGAG 50

RESULT 11
US-10-417-375A-79/c
; Sequence 79, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 54303
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-417-375A-79

Query Match 60.8%; Score 31; DB 6; Length 54303;
Best Local Similarity 87.2%; Pred. No. 0.5;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAG 39
||| | || | |||||||||||||||||||||||||||||
Db 51400 GAGAAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 51362

RESULT 12
US-10-417-375A-1
; Sequence 1, Application US/10417375A
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/417,375A
; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 310122
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(310122)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-1

Query Match 60.8%; Score 31; DB 6; Length 310122;
Best Local Similarity 87.2%; Pred. No. 0.59;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAG 39
|| || |||| ||||||||||||||||||||||| |||
Db 256497 GAAGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAGGAG 256535

RESULT 13
US-10-767-701-15708/c
; Sequence 15708, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 15708
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1381_2
US-10-767-701-15708

Query Match 60.0%; Score 30.6; DB 6; Length 940;
Best Local Similarity 80.0%; Pred. No. 0.43;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
||||| || | || |||||||||||||||||||| ||| |||
Db 699 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 655

RESULT 14
US-10-767-471-10555
; Sequence 10555, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10555
; LENGTH: 34304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(34304)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-767-471-10555

Query Match 60.0%; Score 30.6; DB 6; Length 34304;
Best Local Similarity 80.0%; Pred. No. 0.62;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
|| || |||| |||| |||||||||||||||||| ||| |||
Db 9950 GAAGAAGAAGAAGAAGGGGAGGAGGAGGAGGAGGAGGTGGAA 9994

RESULT 15
US-10-642-946-6
; Sequence 6, Application US/10642946

; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: Genomic Polynucleotide Fragments From Chromosome 7
; FILE REFERENCE: JR-14,000-US
; CURRENT APPLICATION NUMBER: US/10/642,946
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/957,956
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: US 60/234,422
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 45980
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-642-946-6

Query Match 60.0%; Score 30.6; DB 6; Length 45980;
Best Local Similarity 80.0%; Pred. No. 0.64;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||| ||||  |||||||| |||||||| ||||| |||   |||
Db       3845 GAGGAAGAAGAAGAAGAGGAAGAGGAGGAAGAGGAGGAGGAGGAA 3889
```

Search completed: March 2, 2004, 11:51:40
Job time : 20.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:30:03 ; Search time 2156 Seconds
(without alignments)
706.387 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930
Perfect score: 51
Sequence: 1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41.6	81.6	1353	29	AY416856	AY416856 Homo sapi
2	40	78.4	1044	13	BQ880026	BQ880026 AGENCOURT
3	38.8	76.1	1347	29	AY416858	AY416858 Mus muscu
4	38.2	74.9	872	29	ECAA2BAR	AL606560 Horse alp
c 5	37.8	74.1	633	9	AL872808	AL872808 AL872808
c 6	37.8	74.1	634	9	AL852740	AL852740 AL852740
c 7	37	72.5	642	14	CF360731	CF360731 822256 MA
8	37	72.5	787	13	BU748295	BU748295 CH3#019_B
c 9	36.4	71.4	770	28	BZ195097	BZ195097 CH230-248
c 10	36.2	71.0	256	14	CA315228	CA315228 UI-M-FW0-
11	36	70.6	490	9	AA896321	AA896321 vy13c07.r
12	36	70.6	763	14	CB625989	CB625989 OSIIEa15O
c 13	36	70.6	822	14	CB625990	CB625990 OSIIEa15O
c 14	35.4	69.4	365	12	BM659898	BM659898 BJP602768
15	35.4	69.4	378	13	BQ294503	BQ294503 Pa002 Per
16	35.4	69.4	399	12	BI961415	BI961415 MONO1_5_C
17	35.4	69.4	446	12	BI961033	BI961033 MONO1_5_C
18	35.4	69.4	447	9	AL842491	AL842491 AL842491
19	35.4	69.4	496	10	AW760336	AW760336 sl49a06.y
c 20	35.4	69.4	512	14	CB272922	CB272922 mai64d07.
c 21	35.4	69.4	552	14	CF795982	CF795982 892192 MA
22	35.4	69.4	556	13	BX669429	BX669429 BX669429
23	35.4	69.4	571	13	BX676418	BX676418 BX676418
c 24	35.4	69.4	586	9	AI451753	AI451753 mb16f09.y
c 25	35.4	69.4	608	14	CF367914	CF367914 852497 MA
c 26	35.4	69.4	673	14	CF792336	CF792336 885253 MA
c 27	35.4	69.4	677	13	BY706040	BY706040 BY706040
28	35.4	69.4	823	28	BZ504700	BZ504700 BONRX59TR
c 29	35.4	69.4	1080	11	AK005900	AK005900 Mus muscu
c 30	35.4	69.4	1595	11	AK008242	AK008242 Mus muscu
31	35	68.6	304	14	CA618111	CA618111 wl1n.pk00
c 32	35	68.6	528	28	AZ993348	AZ993348 2M0278A22
c 33	35	68.6	617	10	BF220068	BF220068 601296979
c 34	35	68.6	627	10	AW388194	AW388194 MR4-ST012
35	35	68.6	1009	29	CNS04V62	AL308675 Tetraodon
36	34.8	68.2	464	9	AL791191	AL791191 AL791191
37	34.8	68.2	648	9	AL652867	AL652867 AL652867
c 38	34.8	68.2	649	9	AL848797	AL848797 AL848797
39	34.8	68.2	861	13	BX736262	BX736262 BX736262
c 40	34.8	68.2	891	13	BX694066	BX694066 BX694066
c 41	34.8	68.2	895	13	BX771143	BX771143 BX771143
c 42	34.8	68.2	899	9	AL970754	AL970754 AL970754
43	34.6	67.8	354	14	CB961043	CB961043 AGENCOURT
c 44	34.6	67.8	411	14	CD565314	CD565314 B0493A11-
c 45	34.6	67.8	516	14	CA567661	CA567661 K0417C11-

ALIGNMENTS

RESULT 1
AY416856
LOCUS AY416856 1353 bp DNA linear GSS 12-DEC-2003
DEFINITION Homo sapiens HCM6030 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY416856
VERSION AY416856.1 GI:39772816
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1353)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1353)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

```
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1353
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>1353
                     /locus_tag="HCM6030"
ORIGIN

  Query Match            81.6%;  Score 41.6;  DB 29;  Length 1353;
  Best Local Similarity  91.7%;  Pred. No. 11;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              || ||  |  |||||||||||||||||||||||||||||||||||||
Db        892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 939


RESULT 2
BQ880026
LOCUS       BQ880026               1044 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8113358 Lupski_dorsal_root_ganglion Homo sapiens cDNA
            clone IMAGE:6179035 5', mRNA sequence.
ACCESSION   BQ880026
VERSION     BQ880026.1  GI:22272034
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1044)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13559  row: i  column: 20
            High quality sequence stop: 430.
FEATURES             Location/Qualifiers
     source          1. .1044
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6179035"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies."
ORIGIN

  Query Match            78.4%;  Score 40;  DB 13;  Length 1044;
  Best Local Similarity  98.1%;  Pred. No. 23;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 GAGGATGAAGCTGAAGA-GGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        417 GAGGATGAAGCTGAAGAGGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 468


RESULT 3
AY416858
LOCUS       AY416858               1347 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM6030 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY416858
VERSION     AY416858.1  GI:39772818
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1347)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1347)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1347
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>1347
                     /locus_tag="HCM6030"
ORIGIN

  Query Match            76.1%;  Score 38.8;  DB 29;  Length 1347;
  Best Local Similarity  86.0%;  Pred. No. 43;
  Matches   43;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA 50
              ||| | | ||||||||||||| || ||||||| |||||| ||||||||||
Db        883 GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA 932


RESULT 4
ECAA2BAR
LOCUS       ECAA2BAR               872 bp    DNA     linear   GSS 14-SEP-2001
DEFINITION  Horse alpha2 adrenergic receptor gene fragment probably subtype b,
            genomic survey sequence.
ACCESSION   AL606560
VERSION     AL606560.1  GI:15591917
KEYWORDS    GSS; Alpha2 adrenergic receptor gene.
SOURCE      Equus caballus (horse)
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 872)
  AUTHORS   Hunter,C. and Elgar,G.
  TITLE     Alpha2 adrenergic receptor gene
  JOURNAL   Unpublished
```

```
REFERENCE   2  (bases 1 to 872)
  AUTHORS   Hunter,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. UK Email:
            biohelp@hgmp.mrc.ac.uk
FEATURES             Location/Qualifiers
     source          1. .872
                     /organism="Equus caballus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9796"
ORIGIN

  Query Match             74.9%;  Score 38.2;  DB 29;  Length 872;
  Best Local Similarity   84.3%;  Pred. No. 55;
  Matches   43;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
              ||||| || |  || ||||||||||||| |||||||||||||| || |||
Db        592 GAGGAAGAGGAGGAGGAGGAGGAGGAGGGGGAGGAAGAGTGTGAGCCTCAG 642


RESULT 5
AL872808/c
LOCUS       AL872808                633 bp    mRNA    linear   EST 03-DEC-2003
DEFINITION  AL872808 XGC-egg Silurana tropicalis cDNA clone TEgg106k18 5', mRNA
            sequence.
ACCESSION   AL872808
VERSION     AL872808.2  GI:38666205
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 633)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22893073.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg106k18.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .633
                     /organism="Silurana tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg106k18"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             74.1%;  Score 37.8;  DB 9;  Length 633;
  Best Local Similarity   85.7%;  Pred. No. 64;
  Matches   42;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              | |||||||| ||||||||| || |||||||| || ||||||||||| |
Db        559 GTGGATGAAGATGAAGAGGAAGATGAGGAGGATGAGGAGTGTGAACCAC 511


RESULT 6
AL852740/c
LOCUS       AL852740                634 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AL852740 XGC-egg Silurana tropicalis cDNA clone TEgg015d14 5', mRNA
            sequence.
ACCESSION   AL852740
VERSION     AL852740.2  GI:38563553
KEYWORDS    EST.
SOURCE      Silurana tropicalis (western clawed frog)
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 634)
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
COMMENT     On Sep 15, 2002 this sequence version replaced gi:22872961.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TEgg015d14.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES             Location/Qualifiers
     source          1. .634
                     /organism="Silurana tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TEgg015d14"
                     /dev_stage="egg"
                     /lab_host="Escherichia coli XL1-blue"
                     /clone_lib="XGC-egg"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from egg.
                     EcoRI-NotI cut cDNA was then ligated into pCS107 with
                     EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

  Query Match             74.1%;  Score 37.8;  DB 9;  Length 634;
  Best Local Similarity   85.7%;  Pred. No. 64;
  Matches   42;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              | |||||||| ||||||||| || |||||||| || ||||||||||| |
Db        204 GTGGATGAAGATGAAGAGGAAGATGAGGAGGATGAGGAGTGTGAACCAC 156


RESULT 7
CF360731/c
LOCUS       CF360731                642 bp    mRNA    linear   EST 25-AUG-2003
DEFINITION  822256 MARC 3PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION   CF360731
VERSION     CF360731.1  GI:34158729
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 642)
```

```
  AUTHORS   Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,
            Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.
  TITLE     A second set of porcine ESTs from a pooled-tissue normalized
            library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: SRG8014  row: O  column: 4
            Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 3PIG"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including brain, liver, muscle, placenta/endometrium,
                     ovary, testes, and bone marrow."
ORIGIN

  Query Match             72.5%;  Score 37;  DB 14;  Length 642;
  Best Local Similarity   88.9%;  Pred. No. 96;
  Matches   40;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||| |||| |||||||||||| |||||||| |||||| |||||
Db        377 GAGGAGGAAGATGAAGAGGAGGAAGAGGAGGAAGAAGAGAGTGAA 333


RESULT 8
BU748295
LOCUS       BU748295                 787 bp    mRNA    linear   EST 10-OCT-2002
DEFINITION  CH3#019_B01T7 Canine heart normalized cDNA Library in pBluescript
            Canis familiaris cDNA clone CH3#019_B01 5', mRNA sequence.
ACCESSION   BU748295
VERSION     BU748295.1  GI:23700479
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 787)
  AUTHORS   Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
  TITLE     Expressed sequence tags from Canine heart
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: CH3#019_B01T3
            Contact: George AL
            Division of Genetic Medicine
            Vanderbilt University
            529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
            Tel: 615 936 2660
            Fax: 615 936 2661
            Email: al.george@vanderbilt.edu
            Insert Length: 1072   Std Error: 0.00
            Seq primer: T7: TAATACGACTCACTATAGGG
            High quality sequence start: 41
            High quality sequence stop: 785.
FEATURES             Location/Qualifiers
     source          1. .787
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="CH3#019_B01"
                     /tissue_type="heart"
                     /cell_type="heart"
                     /dev_stage="mixed developmental stages (adult, 30 day - 40
                     day fetal)"
                     /clone_lib="Canine heart normalized cDNA Library in
                     pBluescript"
                     /note="Organ: heart; Vector: pBluescript; Site_1: 5' of
                     vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
                     dog heart (adult, 30 day - 40 day fetal), right and left
                     atria and ventricle. Dog breed - mixed (beagle, German
                     shepherd,  pointer, Irish setter). Library construction:
                     oligo-dT primed"
ORIGIN

  Query Match             72.5%;  Score 37;  DB 13;  Length 787;
  Best Local Similarity   88.9%;  Pred. No. 99;
  Matches   40;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              || || ||||| |||||||||||||||||||||||||||  ||||
Db         41 GATGAAGAAGCAGAAGAGGAGGAGGAGGAGGAAGAGGATGAA 85


RESULT 9
BZ195097/c
LOCUS       BZ195097                 770 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-248P14.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-248P14, genomic survey sequence.
ACCESSION   BZ195097
VERSION     BZ195097.1  GI:23853149
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-248P14.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 248  row: P  column: 14
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-248P14"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN
```

```
  Query Match             71.4%;  Score 36.4;  DB 28;  Length 770;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+02;
  Matches   40;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAAC 46
              ||||| || |  ||||||||||||||||||||||||||| | ||||
Db        172 GAGGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAAGAGGGAGAAC 127


RESULT 10
CA315228/c
LOCUS       CA315228                256 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-FW0-cbi-b-15-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
            IMAGE:6809872 5', mRNA sequence.
ACCESSION   CA315228
VERSION     CA315228.1  GI:24533352
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
             The following repetitive elements were found in this cDNA
            sequence: 37-156, >(GGA)n#Simple_repeat (matched compliment)
            82-200, >(GAA)n#Simple_repeat (matched compliment) 201-254,
            >(GGA)n#Simple_repeat (matched compliment)
            Seq primer: pYX-5.
FEATURES              Location/Qualifiers
     source           1. .256
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:6809872"
                      /tissue_type="whole brain"
                      /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                      /lab_host="DH10B (T1 phage resistant)"
                      /clone_lib="NIH_BMAP_FW0"
                      /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                      Site_2: Not I; The library was constructed according
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. Denatured RNA was size fractionated on a 1% agarose
                      gel. First strand cDNA synthesis was primed with oligo-dT
                      primer containing a Not I site. Double strand cDNA was
                      size selected according to mRNA size fraction, ligated
                      with EcoR I adaptor, digested with NotI and then cloned
                      directionally into pYX-Asc vector. The library tag
                      sequence located between the Not I site and the polyA tail
                      is AGCGAGACAG. This library was created for the University
                      Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                      Developing Mouse Nervous System', supported by National
                      Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                      program coordinator."
ORIGIN

  Query Match             71.0%;  Score 36.2;  DB 14;  Length 256;
  Best Local Similarity   83.7%;  Pred. No. 1.3e+02;
  Matches   41;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
              ||||| ||||  || ||||||||||||||||||| |||||  | ||||
Db         65 GAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGATAGCCCC 17


RESULT 11
AA896321
LOCUS       AA896321                490 bp    mRNA    linear   EST 06-APR-1998
DEFINITION  vy13c07.r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
            clone IMAGE:1295340 5' similar to gb:X56135 Mouse mRNA for
            prothymosin alpha (MOUSE);, mRNA sequence.
ACCESSION   AA896321
VERSION     AA896321.1  GI:3032714
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:676388
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 348.
FEATURES              Location/Qualifiers
     source           1. .490
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /db_xref="taxon:10090"
                      /clone="IMAGE:1295340"
                      /tissue_type="macrophage"
                      /dev_stage="WEHI-3 cell line"
                      /lab_host="SOLR (kanamycin resistant)"
                      /clone_lib="Stratagene mouse macrophage (#937306)"
                      /note="Organ: blood; Vector: pBluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                      Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
                      Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                      3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

  Query Match             70.6%;  Score 36;  DB 9;  Length 490;
  Best Local Similarity   88.6%;  Pred. No. 1.5e+02;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              ||||| |||| ||||||||| |||||||||||||||||  ||||
Db         72 GAGGAAGAAGGTGAAGAGGAAGAGGAGGAGGAGGAAGAAGGTGA 115


RESULT 12
CB625989
LOCUS       CB625989                763 bp    mRNA    linear   EST 08-APR-2003
DEFINITION  OSIIEa15O13.f OSIIEa Oryza sativa (indica cultivar-group) cDNA
            clone OSIIEa15O13 5', mRNA sequence.
ACCESSION   CB625989
VERSION     CB625989.1  GI:29620978
KEYWORDS    EST.
```

```
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 15  row: O  column: 13
            Seq primer: gta aaa cga cgg cca gtg.
FEATURES            Location/Qualifiers
     source         1. .763
                    /organism="Oryza sativa (indica cultivar-group)"
                    /mol_type="mRNA"
                    /cultivar="IR36"
                    /db_xref="taxon:39946"
                    /clone="OSIIEa15O13"
                    /tissue_type="Leaf"
                    /dev_stage="3 week"
                    /lab_host="DH10B"
                    /clone_lib="OSIIEa"
                    /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                    XhoI; Lesion Mimic SPL 11"
ORIGIN

  Query Match             70.6%;  Score 36;  DB 14;  Length 763;
  Best Local Similarity   88.6%;  Pred. No. 1.6e+02;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              ||||| ||||  |||||||||||||||||||||||||| | ||
Db        601 GAGGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAAGAGAGCGA 644


RESULT 13
CB625990/c
LOCUS       CB625990                822 bp    mRNA    linear   EST 08-APR-2003
DEFINITION  OSIIEa15O13.r OSIIEa Oryza sativa (indica cultivar-group) cDNA
            clone OSIIEa15O13 3', mRNA sequence.
ACCESSION   CB625990
VERSION     CB625990.1  GI:29620979
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
  ORGANISM  Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
  TITLE     Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
            PCR PRimers
            FORWARD: gta aaa cga cgg cca gtg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 15  row: O  column: 13
            Seq primer: gga aac agc tat gac cat g.
FEATURES            Location/Qualifiers
     source         1. .822
                    /organism="Oryza sativa (indica cultivar-group)"
                    /mol_type="mRNA"
                    /cultivar="IR36"
                    /db_xref="taxon:39946"
                    /clone="OSIIEa15O13"
                    /tissue_type="Leaf"
                    /dev_stage="3 week"
                    /lab_host="DH10B"
                    /clone_lib="OSIIEa"
                    /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
                    XhoI; Lesion Mimic SPL 11"
ORIGIN

  Query Match             70.6%;  Score 36;  DB 14;  Length 822;
  Best Local Similarity   88.6%;  Pred. No. 1.7e+02;
  Matches   39;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
              ||||| ||||  |||||||||||||||||||||||||| | ||
Db        594 GAGGAAGAAGAAGAAGAGGAGGAGGAGGAGGAGGAAGAGAGCGA 551


RESULT 14
BM659898/c
LOCUS       BM659898                365 bp    mRNA    linear   EST 27-FEB-2002
DEFINITION  BJP602768646.R1 CSEQFXL38 pig thyroid and parathyroid Sus scrofa
            cDNA, mRNA sequence.
ACCESSION   BM659898
VERSION     BM659898.1  GI:18962904
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 365)
  AUTHORS   Adelson,D.L. and Gill,C.A.
  TITLE     Porcine ESTs
  JOURNAL   Unpublished (2002)
COMMENT     Contact: David L. Adelson
            Animal Breeding and Genetics
            Texas A&M University
            Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
            USA
            Tel: 9798452616
            Fax: 9798456970
            Email: david.adelson@tamu.edu.
FEATURES            Location/Qualifiers
     source         1. .365
                    /organism="Sus scrofa"
                    /mol_type="mRNA"
                    /db_xref="taxon:9823"
                    /clone_lib="CSEQFXL38 pig thyroid and parathyroid"
                    /note="Organ: thyroid and parathyroid gland; Vector:
                    pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5'
                    of the insert (5'-NNN. . .NNNinsert)
                    GCGAATTGGAGCTCCACCGCGGTGGCGGCCGCGGCTCGAG. Sequence 3' of
                    the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.
                    non-normalized library, sequenced 3' with M13R primer."
ORIGIN

  Query Match             69.4%;  Score 35.4;  DB 12;  Length 365;
  Best Local Similarity   86.7%;  Pred. No. 2e+02;
  Matches   39;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
```

```
Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||| |||| ||| |||||||| |||||||| |||||| |||||
Db        149 GAGGAGGAAGATGAGGAGGAGGAAGAGGAGGAAGAAGAGAGTGAA 105


RESULT 15
BQ294503
LOCUS       BQ294503                 378 bp    mRNA    linear   EST 15-MAY-2002
DEFINITION  Pa002 Periplaneta americana Lambda Express library Periplaneta
            americana cDNA clone 5, mRNA sequence.
ACCESSION   BQ294503
VERSION     BQ294503.1  GI:20803437
KEYWORDS    EST.
SOURCE      Periplaneta americana (American cockroach)
  ORGANISM  Periplaneta americana
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
            Blattidae; Periplaneta.
REFERENCE   1  (bases 1 to 378)
  AUTHORS   Zhou,Z.W., Liu,Z.G. and Gao,B.
  TITLE     The construction of Periplaneta americana nymph cDNA library and
            lgG4 immunology screen
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Zhou,Z.W.
            Immnology Department
            Jiang Xi Medical College
            106, Bayi Street, Nanchang, Jiangxi, P.R.C.
            Tel: 86-0791-6363001
            Email: Zhouzhenwen28@hotmail.com.
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Periplaneta americana"
                     /mol_type="mRNA"
                     /db_xref="taxon:6978"
                     /clone="5"
                     /tissue_type="whole body"
                     /dev_stage="nymph"
                     /lab_host="E.coli NM522"
                     /clone_lib="Periplaneta americana Lambda Express library"
                     /note="Vector: Lambda Excell; These sequences were
                     screened by cockroach sensitive patients' IgG4  serum "
ORIGIN

  Query Match           69.4%;  Score 35.4;  DB 13;  Length 378;
  Best Local Similarity  86.7%;  Pred. No. 2e+02;
  Matches   39;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
              ||||| |||||||||||| |||||||||||| |||||||||   |||
Db        159 GAGGAGGAAGCTGAAGAAGAGGAGGAGGAAGAGGAAGAGGAAGAA 203


Search completed: March  2, 2004, 08:34:35
Job time : 2156 secs
```